

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2005, 05:59:01 ; Search time 17 Seconds
(without alignments)
2190.346 Million cell updates/sec

Title: US-10-800-249-2
Perfect score: 2081
Sequence: 1 MNRHLLQDHFLEIDKKNCCV.....KGHCHOEPASLEKOLGCCIE 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1990	95.6	387	2 I69202	G protein-coupled
2	431	20.7	362	2 S33733	G protein-coupled
3	415	19.9	373	2 JC4162	p2y receptor - bov
4	407	19.6	373	2 JC4737	G protein-coupled
5	351.5	16.9	308	2 I50241	G protein-coupled
6	350.5	16.8	364	2 JQ1488	bradykinin B2 rece
7	348.5	16.7	370	2 JC5549	heptahelical p2y5-
8	348	16.7	328	2 I55450	G protein-coupled
9	341	16.4	399	2 I48705	proteinase activat
10	339.5	16.3	344	2 I09508	intron 17 purinerg
11	337	16.2	373	2 A47556	ATP receptor P2u -
12	337	16.2	397	2 S66518	proteinase-activat
13	333	16.0	342	2 A40191	platelet-activatin
14	330.5	15.9	384	2 A47249	brain-specific som
15	326.5	15.7	366	1 OORT82	bradykinin recepto
16	326	15.7	380	2 JC2338	kappa opioid recep
17	325	15.6	380	2 A55259	kappa opioid recep
18	324.5	15.6	380	2 S31613	kappa opioid recep
19	323	15.5	328	2 JC4800	p2y6 receptor - hu
20	323	15.5	365	2 S68679	G protein-coupled
21	323	15.5	425	2 A37912	thrombin receptor
22	322.5	15.5	390	2 A48227	kappa opioid recep
23	322	15.5	388	2 JN0605	somatostatin recep
24	321	15.4	420	2 I51667	thrombin receptor
25	320	15.4	366	2 I49519	bradykinin B2 rece
26	317	15.2	369	2 JC5068	G protein-coupled
27	317	15.2	391	2 C41795	somatostatin recep
28	317	15.2	391	2 A39297	somatostatin recep
29	316	15.2	391	2 A41795	somatostatin recep

30	315.5	15.2	369	2 B41795	somatostatin recep
31	314.5	15.1	342	2 SI3638	platelet-activatin
32	314.5	15.1	369	2 JC2083	somatostatin recep
33	314.5	15.1	380	2 JC2434	kappa opioid recep
34	314.5	15.1	384	2 JC4629	somatostatin recep
35	313.5	15.1	369	2 A45291	somatostatin recep
36	313.5	15.1	432	2 A43448	thrombin receptor
37	310	14.9	341	2 S63666	platelet activatin
38	310	14.9	341	2 S43252	platelet-activatin
39	309	14.8	398	2 A57510	mu opioid receptor
40	308.5	14.8	398	2 I56517	mu opioid receptor
41	307.5	14.8	364	2 JN0763	somatostatin recep
42	307	14.8	418	2 A46226	somatostatin recep
43	306	14.7	355	2 I49339	macrophage inflam
44	305.5	14.7	372	2 I38532	delta opioid recep
45	305	14.7	355	2 A45177	chemokine (C-C) re

ALIGNMENTS

RESULT 1

I69202
G protein-coupled receptor HM74 - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I69202
R;Nomenclature: H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemokine (C-C) re
A;Reference number: I54751; MUID:94092629; PMID:7505609.
A;Accession: I69202
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: UNIPROT:P49019; GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867
C;Genetics:
A;Gene: HM74
C;Superfamily: G protein-coupled receptor 4

Query Match	95.6%	Score 1990;	DB 2;	Length 387;
Best Local Similarity	95.9%	Pred. No. 3.6e-170;		
Matches 371;	Conservative 6;	Mismatches 10;	Indels 0;	Gaps 0;
Qy	1	MNRHHLQDHFLEIDKKNCCVFRDDFI	VKVLPPVLGLEFI	FGLLGNGLALMIFCFHLKSWK 60
Db	1	MNRHHLQDHFLEIDKKNCCVFRDDFI	AKVLPVVLGLEFI	FGLLGNGLALMIFCFHLKSWK 60
Qy	61	SSRIFLNLAVADFLIILICLPFLMDNVYRRWDWKFGDIP	PCRLMLFMLAMNRQGSII	FLTV 120
Db	61	SSRIFLNLAVADFLIILICLPFVMDYVYRRSDWNFGDIP	PCRLVLFMPAMNRQGSII	FLTV 120
Qy	121	VAVDRYFRVPHHAKNISNRTAAIISCLLWGTIGLT	TVHLLKKKKPIONGGANLCSF	180
Db	121	VAVDRYFRVPHHAKNISNRTAAIISCLLWGTIGLT	TVHLLKKKLLIIONGPANVCISF	180
Qy	181	SICHTFOWHEAMFLLEPFLPLGIILFCSARIINSLRQMDR	HAKIKRAITFIWVAIVF	240
Db	181	SICHTFRWHEAMFLLEPFLPLGIILFCSARIINSLRQMDR	HAKIKRAITFIWVAIVF	240
Qy	241	VICFLPSVVVRIIRIFWLLHSTGTQNCVYRSVDLAFFIT	LSFTYMNMLDPVVYFSSPS	300
Db	241	VICFLPSVVVRIIRIFWLLHSTGTQNCVYRSVDLAFFIT	LSFTYMNMLDPVVYFSSPS	300
Qy	301	FPNFFSTLIINRCLOKMTGEPDNNRSTSVELTGDPNKTR	GAPEALMANSCEPWPSPYLGP	360
Db	301	FPNFFSTLIINRCLOKMTGEPDNNRSTSVELTGDPNKTR	GAPEALMANSCEPWPSPYLGP	360
Qy	361	TSNNHKKGHCHOEPASLEKOLGCCIE	387	
Db	361	TSNNHKKGHCHOEPASLEKOLGCCIE	387	

A;Reference number: I48705; MUID:95197620; PID:7890726

A;Accession: I48705

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-399 <RES>

A;Cross-references: UNIPROT:P55086; EMBL:Z48043; NID:G663020; PIDN:CAA88097.1; PID:G6630

C;Superfamily: ATP receptor P2u

Query Match 16.4%; Score 341; DB 2; Length 399;
Best Local Similarity 30.5%; Pred. No. 9.8e-23;
Matches 92; Conservative 59; Mismatches 127; Indels 24; Gaps 9;

Qy 13 IDKNCCVFRDDFIVKVLPPVLGIEFIFGLLGNLALWIFCFHLKSKWSSRIEFLNLA 72
Db 63 IDEFSASITKGLTVPVVIIVFVIGLPSNGMALWIFLRTKXKHPAIVMANALA 122
Qy 73 DFLLIICLPFLMDNYRRWDKFGDIPCRMLFMLAMNRQGSIFLTWADVFRVVP 132
Db 123 DLSVINPEPLKISHLGNWVGEALCKVLIGFFGNMYCSILFMTCLSVQRVWVNP 182
Qy 133 HHALNKISNRTAAIISCLLWGITITGLTVHLLKKKPIQNGGANICSSFSICHTPQHEAM 192
Db 183 MGHPKKNAN-IAVGVSLAIWLILFVLVPMQTIIVPALNI-----TTCDDVLPPEVL 237
Qy 193 F--LLEFPLP--GIILP-----CSARI--IWSLRQRMDBHA--KKRAITFIMVVAIV 239
Db 238 VGDNFNYFLSAIGVLFPAALLTASAYVLMIKTLRSSAMDEHSEKKQRAIRLIITVLM 297
Qy 240 FVICFLSVVVRIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVYVYFSSP 299
Db 298 YFICFAPSNNLLVHHYFLIKTQ--RQSHVY---ALYDVALCLSLNCSIDPFVYFVSK 351
Qy 300 SF 301
Db 352 DF 353

RESULT 10

T09508

Intron 17 purinergic receptor P2Y5 - human

N;Alternate names: G-protein coupled receptor

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

R;Bohm, S.K.; Trumpff, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.

submitted to the EMBL Data Library, April 1997

A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob

A;Reference number: Z16705

A;Accession: T09508

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-344 <BOH>

A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:G2232068; PID:G2232069

C;Genetics:

A;Map position: 13

C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 16.3%; Score 339.5; DB 2; Length 344;
Best Local Similarity 28.2%; Pred. No. 1.1e-22;
Matches 83; Conservative 65; Mismatches 135; Indels 11; Gaps 7;

Qy 19 CVFRDDFIVKVLPPVLGIEFIFGLLGNLALWIFCFHLKSKWSSRIEFLNLA 78
Db 9 CFYNDSEKTYLYGCMFWSVFLGLVSNCAIYIFICVLKVRNETTTWINLAMSDDLFPV 68
Qy 79 CLPFLMDNYRRWDKFGDIPCRMLFMLAMNRQGSIFLTWADVFRVFRVPHHALNK 138
Db 69 TLPRIFVFYFTR--NWPFCDLLCKISVLMFYTNMYGSIILFLTCISVDRAFLAIVYFPSKTL 127
Qy 139 ISNRTAAIISCLLWGITITGLTVHLLKKKPIQNGGANIC--SIFHTFQWHEAMF 193
Db 128 RTRKNAKIVCTGVVLTIGGAPAVFVQSTHSQGNASEACFENFPPEATWTKYLSRIVIF 187

Qy 194 --LLEFPLPGLIIFCSARIISLRQRMDBHAKIK--RAITFIMVVAIVFVICFLPSVV 249
Db 188 IEIVGFFIPLILNWTGSSVMVLKTLTKPVLTSRSKINKTKVKMLFVHLIIFCFCFVP--YN 246
Qy 250 VRIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVYVYFSSPSFPN 303
Db 247 INILYSLVTRTQTFVNCVVAAVTRWYPIITLCIAVSNCCFDPVYIFTSDTIQN 300

RESULT 11

A47556

ATP receptor P2u - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: A47556

R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A;Reference number: A47556; MUID:93281707; PMID:7685114

A;Accession: A47556

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-373 <LUS>

A;Cross-references: UNIPROT:P35383; GB:L14751; NID:G309457; PIDN:AAA39871.1; PID:G309458

C;Superfamily: ATP receptor P2u

C;Keywords: transmembrane protein

Query Match 16.2%; Score 337; DB 2; Length 373;
Best Local Similarity 27.5%; Pred. No. 2.1e-22;
Matches 97; Conservative 56; Mismatches 158; Indels 42; Gaps 6;

Qy 19 CVFRDDFIVKVLPPVLGIEFIFGLLGNLALWIFCFHLKSKWSSRIEFLNLA 78
Db 25 CRNEDEKXYVLLPVSYGVVGVCLNVALYIFLCRLKTNASTTYMFLAVSDSLVAA 84
Qy 79 CLPFLMDNYRRWDKFGDIPCRMLFMLAMNRQGSIFLTWADVFRVFRVPHHALNK 138
Db 85 SLPLLYYYARGDHPFESTVLCKLVRFYTNLYCSILFLTCISVHRCLGLVLRPLSLRW 144
Qy 139 ISNRTAAIISCLLWGITITGLTVHLLKKKMPIONGANLCSFS---ICTFQWHEAMFL 194
Db 145 GRARYARRVAAVVWLVLACQAPVLYVTTSVRGTRITCHDTSARELFESHVAYSSVMLG 204
Qy 195 LEFPLPGLIIFCSARIISLRQRMDBR-----HAKIKRAITFIMVVAIVFVICF 244
Db 205 LLFAVPSVILVC-----YVMARRLLKPAYITGGLPRAKRKSVRTIALVLA--VFALCF 258
Qy 245 LPSVVVRIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVYVYFSSPSFPN 304
Db 259 LPFHVT--RTLYYSFRSLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAQRLVRF 316
Qy 305 FSTL-----INRCLORKMTGEPPDNNRSTSVELTGDPNK 337
Db 317 ARDAKPTEPTPSQARKLGLHRPNRTVRKDJUSVSSDDSRRTTESTPAGSETK 369

RESULT 12

S66518

Proteinase-activated receptor 2 precursor - human

C;Species: Homo sapiens (man)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S66518; S64709; G02131

R;Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin, J.

Eur. J. Biochem. 232, 84-89, 1995

A;Title: Molecular cloning and functional expression of the gene encoding the human prot

A;Reference number: S66518; MUID:96048032; PMID:7556175

A;Accession: S66518

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-397 <NYS>

A;Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:G1008084; PIDN:CAA90280.1; PID:G100

R;Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn

Biochem. J. 314, 1009-1016, 1996
A;Title: Molecular cloning, expression and potential functions of the human proteinase-
A;Reference number: S64709; MUID:96177879; PMID:8615752
A;Accession: S64709
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137, 'A', 139-397 <BOE>
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AA847871.1; PID:g1041729
A;Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residue 2
R;Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A;Reference number: H00822
A;Accession: G02131
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 28-397 <KAH>
A;Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540
C;Genetics:
A;Map position: 5q13
A;Introns: 28/1
C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 16.2%; Score 337; DB 2; Length 397;
Best Local Similarity 26.2%; Pred. No. 2.2e-22;
Matches 100; Conservative 68; Mismatches 153; Indels 60; Gaps 9;

QY 13 IDKNCOCVFRDPIVKVLPVLGLETFGLGLGLALWIFCFHLKSKWSSRIFLFNLA 72
DB 61 VDFESASVLTGKLTTFPIVTVIVFVGLPSNGMALWFLPRTKKKHPAVIMANLALA 120

QY 73 DFLLIICLPFLMNYVRWDKGDIPCLRLMLFWMANRQSGIIFLTVAVDYFRVWHP 132
DB 121 DLLSVTFWFLPKIAHYHGNWMIYGEALCNVLIGFFYGNMYCSILFTWCLSVQRYWIVNP 180

QY 133 HHALNKISNTAAIISCLMGITIGTIVHLKKMKPIONGANLCSFSFICHTFQWHEAM 192
DB 181 MGHSRKAN-IAIGISLAIWLLILLVTIPLYVVKQIFIPALNI-----TTCHDVLPEQLL 235

QY 193 F--LLEFFFLP--GILF-----CSARI--IWSLRQQRDHA--KIKRAITFIMVVAIV 239
DB 236 VGDMFNYFLSLAIGVLFPAFLTASAYVLMIRLMRSSAMDENSEKKRKAIRKILVTVLAM 295

QY 240 FVICFLPSVVRIIFWLLHTSGTQCEVRSVDLAFFITLSTYWNMLDPVYVFPSP 299
DB 296 YLICFTPSNLLLVHVFLIKSQGSH-----VYALYIVALCLSTLNSCIDPFVYFVSH 349

QY 300 SFPNFFSTLINRCLQRKWTGCPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLG 359
DB 350 DFRDH-----AKNALLCRSVRTVKQMQVS 373

QY 360 PTSNNHSGKHGHQCEPASLEK 380
DB 374 LTSKHSRKSXSSXSSSTTVK 394

RESULT 13
A40191
platelet-activating factor receptor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text change 09-Jul-2004
C;Accession: A40191; JH0479; A41079; JCI359; A42831; I51923
R;Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell su
A;Reference number: A40191; MUID:92250505; PMID:1374385
A;Accession: A40191
A;Molecule type: mRNA
A;Residues: 1-342 <KUN>
A;Cross-references: UNIPROT:P25105; GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.

Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A;Title: Characterization of a human cDNA that encodes a functional receptor for platelet
A;Reference number: JH0479; MUID:92028922; PMID:1656963
A;Accession: JH0479
A;Molecule type: mRNA
A;Residues: 1-342 <YER>
A;Cross-references: GB:M80436; NID:gi89537; PIDN:AAA60001.1; PID:gi89538
A;Experimental source: granulocyte, cell line HL-60 all
R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Sey
J. Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating factor receptor from hu
A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <NAK>
A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BA01050.1; PID:g219976
R;Sugimoto, T.; Tsuchimoto, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A;Title: Molecular cloning and characterization of the platelet-activating factor recept
A;Reference number: JCI359; MUID:93112021; PMID:1281995
A;Accession: JCI359
A;Molecule type: mRNA
A;Residues: 1-315, 'N', 317-342 <SUG>
A;Experimental source: heart
A;Note: the authors translated the codon AAT for residue 316 as Lys
R;Seifried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns
A;Reference number: A42831; MUID:92347886; PMID:1322356
A;Accession: A42831
A;Molecule type: DNA
A;Residues: 1-226, 'TG', 229-342 <SEY>
A;Cross-references: GB:M88177; NID:gi90697; PIDN:AAA6024.1; PID:gi90698
A;Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for an int
A;Reference number: I51923; MUID:93192035; PMID:8383507
A;Accession: I51923
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-342 <RES>
A;Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
C;Genetics:
A;Gene: GDB:PTAFR
A;Cross-references: GDB:128806; OMIM:173393
A;Map position: lp35-1p34.3
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;17-38/Domain: transmembrane #status predicted <TRI>
F;54-75/Domain: transmembrane #status predicted <TII>
F;92-113/Domain: transmembrane #status predicted <III>
F;134-155/Domain: transmembrane #status predicted <TIV>
F;184-205/Domain: transmembrane #status predicted <TRV>
F;233-253/Domain: transmembrane #status predicted <TVI>
F;277-297/Domain: transmembrane #status predicted <VII>

Query Match 16.0%; Score 333; DB 2; Length 342;
Best Local Similarity 27.9%; Pred. No. 4.3e-22;
Matches 89; Conservative 58; Mismatches 140; Indels 32; Gaps 8;

QY 24 DRIKVLPPVLGLETFGLGLGLALWIFC--FHLKSWSSRIFLFNLAVALLELLICLP 81
DB 12 EFRYTLFPYVYSIIFVLGVANGYVLWVFARLYPCKKFEIKIFMVNLTMADMLFLITLP 71

QY 82 FLMDNVVRWDKFGDIPCLRLMLFWMANRQSGIIFLTVAVDYFRVWHPHNLKISN 141
DB 72 LMIVVYQNGNWLPLFCLNVAACLPFFINTYCSVAELGVITYNRFOAFTPIKTAQANTR 131

QY 142 RTAAIISCLMGITIGTIVHL-----KKXWPIONGANLCSFSF-----ICHTFQ 187
DB 132 KRGISLSLVIVVAIVGAASYFLILDSTNTVPDSAGSNVTRCFEYHEKGSVPVLIHIF- 190

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2005, 05:58:30 ; Search time 59 Seconds
(without alignments)
3358.892 Million cell updates/sec

Title: US-10-800-249-2

Perfect score: 2081.

Sequence: 1 MNRHLDQHFLEIDKKNCCV.....KGHCHEPASLEKOLGCCIE 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1995	95.9	387	QNGE4	Qnge4 homo sapien
2	1990	95.6	387	Q9019	Q9019 homo sapien
3	1935	93.0	363	Q8TDS4	Q8Tds4 homo sapien
4	1591	76.5	360	Q80Z39	Q80z39 rattus norv
5	1577	75.8	360	Q9EP66	Q9ep66 mus musculu
6	1111	53.4	263	Q8NGV8	Q8ngv8 homo sapien
7	900.5	43.3	343	Q881_MOUSE	Q8c131 mus musculu
8	883.5	42.5	346	Q881_HUMAN	Q8bxc0 homo sapien
9	876.5	42.1	346	Q8NXU5	Q8nxu5 homo sapien
10	563	27.1	384	Q8NGW4	Q8ngw4 homo sapien
11	563	27.1	384	Q86WP7	Q86wp7 homo sapien
12	563	27.1	423	Q8TDS5	Q8tds5 homo sapien
13	496.5	23.9	319	Q8NQ20	Q8ngq20 homo sapien
14	494.5	23.8	319	Q931_HUMAN	Q8o270 homo sapien
15	481	23.1	319	Q9JLS1	Q9jls1 mus musculu
16	431	20.7	362	P2YR_CHICK	P34996 gallus gall
17	431	20.7	362	P2YR_MELGA	P34962 meleagris g
18	420	20.2	373	P2YR_RAT	P49651 rattus norv
19	415.5	20.0	347	Q7ZZA4	Q7zza4 brachydanio
20	415	19.9	361	Q90X57	Q90x57 xenopus lae
21	415	19.9	373	P2YR_BOVIN	Q8042 bos taurus
22	413.5	19.9	357	Q9DE05	Q9de05 raja erinac
23	410	19.7	373	P2YR_MOUSE	P49650 mus musculu
24	407	19.6	373	P2YR_HUMAN	P47900 homo sapien
25	407	19.6	373	Q8BMJ5	Q8bmj5 mus musculu
26	406	19.5	373	P2YR_CAVPO	P59902 cavia porce
27	386.5	18.6	349	Q9P852	Q9p852 xenopus tro
28	378.5	18.2	309	GP35_HUMAN	Q9hc97 homo sapien
29	376.5	18.1	394	Q6ZMP9	Q6zmp9 homo sapien
30	374.5	18.0	346	CLT2_HUMAN	Q9n875 homo sapien
31	374	18.0	339	Q6NS65	Q6ns65 mus musculu

32	368	17.7	374	2	O57466	O57466 meleagris g
33	358	17.2	309	1	CLT2_RAT	Q92459 rattus norv
34	358	17.2	537	1	P2Y8_XENLA	P79928 xenopus lae
35	358	17.2	537	2	Q7ZWQ7	Q7zwq7 xenopus lae
36	354.5	17.0	370	2	Q6NSP5	Q6nsp5 homo sapien
37	353.5	17.0	370	1	P2Y9_HUMAN	Q99677 homo sapien
38	352.5	16.9	345	1	CLT2_PIG	Q95n03 sus scrofa
39	351.5	16.9	308	1	P2Y5_CHICK	P32250 gallus gall
40	350.5	16.8	307	2	Q8BS98	Q8bs98 mus musculu
41	350.5	16.8	364	2	Q68DM8	Q68dm8 homo sapien
42	350.5	16.8	391	1	BRB2_HUMAN	P30411 homo sapien
43	350	16.8	367	1	GP17_HUMAN	Q13304 homo sapien
44	349	16.8	361	1	P2Y4_MOUSE	Q91j57 mus musculu
45	348.5	16.7	370	2	Q8BKX1	Q8bkk1 mus musculu

ALIGNMENTS

RESULT 1

ID	QNGE4	PRELIMINARY;	PRT;	387 AA.
AC	QNGE4;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Seven transmembrane helix receptor.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR	EMBL; AB065865; BAC06083.1; -			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0045028; F:purinergic nucleotide receptor activity; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.			
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.			
DR	InterPro; IPR002286; GPCR Rhodpsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PRINTS; PR01157; P2YPURNOCPTR.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
SQ	SEQUENCE 387 AA; 44495 MW; 26433855E85EC81 CRC64;			

Query Match 95.9%; Score 1995; DB 2; Length 387;
Best Local Similarity 96.1%; Pred. No. 7.1e-130;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy	1	MNRHLDQHFLEIDKKNCCVFRDDPIVKVLPVVLGLEFIFGLLGNGLALWIFCFHLKSWK	60
Db	1	MNRHLDQHFLEIDKKNCCVFRDDPIAKVLPVVLGLEFIFGLLGNGLALWIFCFHLKSWK	60
Qy	61	SSRIFFLNLAADVALLIICLPFLMDNVRRWDKFGDIPCLMLFMFLAMNQGSIIIFLTV	120
Db	61	SSRIFFLNLAADVALLIICLPFLMDNVRRWDKFGDIPCLVLFMFAMNQGSIIIFLTV	120
Qy	121	VAVDRYFRVPHHALNKNISNRTAAISCLLWGITGLTVHLLKKKPIONGNLCSSF	180
Db	121	VAVDRYFRVPHHALNKNISNRTAAISCLLWGITGLTVHLLKKKLIQNGPANVCISF	180
Qy	181	SICHTFOWHEAMFLERFFPLGIILFCSARIWSLRQMDRHKAKIKRAITFMVAIVF	240
Db	181	SICHTFRWHEAMFLERFFPLGIILFCSARIWSLRQMDRHKAKIKRAITFMVAIVF	240

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QY 241 VICFLPSVVIRIRIFWLLHTSGTQNCVYRSVDLAPFITLSFTYMSMLDPVYYFSSPS 300
DB 241 VICFLPSVVIRIRIFWLLHTSGTQNCVYRSVDLAPFITLSFTYMSMLDPVYYFSSPS 300
QY 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPALMANSGEPMSPSYLGP 360
QY 361 TSNHSHKKGCHQOEPALEKQGCCIE 387
DB 361 TSNHSHKKGCHQOEPALEKQGCCIE 387

RESULT 2
G09B_HUMAN STANDARD; PRT; 387 AA.
AC P49019;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor GPR109B (G protein-coupled
DE receptor HM74).
GN Name=GPR109B; Synonyms=HM74;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a Ld78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; D10923; BAA01721.1; -
DR PIR; I69202; I69202.
DR HSSP; P34996; IDDO.
DR Genew; HGNC:16824; GPR109B.
DR MIM; 606039; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR000226; GPCR_Rhodpsn.
DR InterPro; IPR002286; P2_puroncptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 28 Extracellular (Potential).
FT TRANSMEM 29 50 1 (Potential).
FT DOMAIN 51 63 Cytoplasmic (Potential).
FT TRANSMEM 64 85 2 (Potential).
FT DOMAIN 86 102 Extracellular (Potential).
FT TRANSMEM 103 123 3 (Potential).
FT DOMAIN 124 142 Cytoplasmic (Potential).
FT TRANSMEM 143 163 4 (Potential).
FT DOMAIN 164 194 Extracellular (Potential).
FT TRANSMEM 195 209 5 (Potential).

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FT DOMAIN 210 236 Cytoplasmic (Potential).
FT TRANSMEM 237 266 6 (Potential). (Potential).
FT DOMAIN 274 298 Extracellular (Potential).
FT TRANSMEM 275 298 7 (Potential).
FT DOMAIN 299 387 Cytoplasmic (Potential).
FT DISULFID 100 177 By similarity.
SQ SEQUENCE 387 AA; 44481 MW; C244F562C2343647 CRC64;

Query Match 95.6%; Score 1990; DB 1; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.6e-129;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHLLQDHFLIEDKKNCVVERDDFTVKVLPVPLGLEFIPLGLNGLALWIFCFHLKSWK 60
DB 1 MNRHLLQDHFLIEDKKNCVVERDDFTAKVLPVPLGLEFIPLGLNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLLIICLPFLMDNYVRRVDMWKFQDIPCLRLMFLMANNRQGSIIFLT 120
DB 61 SSRIFLNLAVADFLLIICLPFVMDYVRRVDMWKFQDIPCLRLVLFWMANNRQGSIIFLT 120
QY 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITITGLTVHLLKKMPTONGGANLCSF 180
DB 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITVGLTVHLLKKLLIQNGPANVCISF 180
QY 181 SICTHFQHEAMFLLEFFLPLGLIILFCSARIISLRSRQROWDRHAKIKRAITFMVVAIV 240
DB 181 SICTHFQHEAMFLLEFFLPLGLIILFCSARIISLRSRQROWDRHAKIKRAITFMVVAIV 240
QY 241 VICFLPSVVIRIRIFWLLHTSGTQNCVYRSVDLAPFITLSFTYMSMLDPVYYFSSPS 300
DB 241 VICFLPSVVIRIRIFWLLHTSGTQNCVYRSVDLAPFITLSFTYMSMLDPVYYFSSPS 300
QY 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPALMANSGEPMSPSYLGP 360
QY 361 TSNHSHKKGCHQOEPALEKQGCCIE 387
DB 361 TSNHSHKKGCHQOEPALEKQGCCIE 387

RESULT 3
Q8TDS4 PRELIMINARY; PRT; 363 AA.
AC Q8TDS4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor HM74a (Seven transmembrane helix
DE receptor).
GN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elshourbagy N.,
RA Eilert M., Ignar D.M., Murdock P.R., Stepkowski K., Green A.,
RA Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA Wilson S., Pike N.B.;
RT "Molecular identification of high and low affinity receptors for
RT nicotinic acid.";
RL J. Biol. Chem. 278:9869-9874(2003).
RN [3]
RP SEQUENCE FROM N.A.
RA Elshourbagy N.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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DR GO: GO:0001614; F:purinergic nucleotide receptor activity; IDA.
 DR InterPro: IPR000216; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 360 AA; 41400 MW; CCCB52A2475777FC CRC64;

Query Match 75.8%; Score 1577; DB 2; Length 360;
 Best Local Similarity 83.1%; Pred. No. 4.7e-101;
 Matches 295; Conservative 19; Mismatches 41; Indels 0; Gaps 0;

QY 8 DHFLETDKKNCCVFRDDFIVKVLPPVLGLFIFGLGNGLALWIFCFHLKSWKSSRIFLP 67
 Db 5 DHFLVINGKNCVFRDNIATKVLPPVLGLFIFGLGNGLALWIFCFHLKSWKSSRIFLP 64
 QY 68 NLAVADFLIIICLPFLMDNVVRWDWKFGDIPCRMLFMLAMNRQSGIIFLTVAVDYRF 127
 Db 65 NLAVADFLIIICLPFLTDNVVHNDWRFGIPCRVLMFLAMNRQSGIIFLTVAVDYRF 124
 QY 128 RVVPHHALKISNRTAAIISCLLWGTTIGLTVHLLKKKMPIONGANLCSFSICHTFO 187
 Db 125 RVVPHHFLNKISNRTAAIISCFGLWLTIGLTVHLLVYTNMTKNGEAYLCSFSICYNFR 184
 QY 188 WHEAMELLEFFFLGLIILCSARIILSLRQDRHAKIKRAITFTIMVAIVFVICFLPS 247
 Db 185 WHDAMELLEFFFLGLIILCSGRIILSLRQDRHAKIKRAINFIMVAIVFVICFLPS 244
 QY 248 VVVRIRIFWLLHSTGTCQNEVRSVDLAFITLSFTYMSMLDPVYVYFSSPSFPNFFST 307
 Db 245 VAVRIRIFWLLYKYNVRNCDIYSSVDLAFITLSFTYMSMLDPVYVYFSSPSFPNFFST 304
 QY 308 LINRCLQRKWTGPDNNRSTSVLTGDPNKTGAPALMANGSPSPYLGPST 362
 Db 305 CINRCLRKTKTGLPDDNNRSTSVLTGDPSTRTSIPGALMADPSPGSPYLASTS 359

RESULT 6
 Q8NGV8 PRELIMINARY; PRT; 263 AA.
 ID Q8NGV8
 AC Q8NGV8
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Seven transmembrane helix receptor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Tsubutani S., Aburatani H., Asai K., Akiyama Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AB065665; BAC05891.1; -
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0045028; F:purinergic nucleotide receptor activity; G- . . ; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR002286; P2_puroceptor.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PRINTS: PR01157; P2YPURNOCPTR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 263 AA; 30289 MW; F96B9F023A5B1F1C1 CRC64;

Query Match 53.4%; Score 1111; DB 2; Length 263;
 Best Local Similarity 98.6%; Pred. No. 5e-69; 2; Indels 0; Gaps 0;
 Matches 205; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRHHLQDHFLIEDKKNCCVFRDDFIVKVLPPVLGLFIFGLGNGLALWIFCFHLKSWK 60
 Db 1 MNRHHLQDHFLIEDKKNCCVFRDDFIVKVLPPVLGLFIFGLGNGLALWIFCFHLKSWK 60
 QY 61 SSRIFLNLAVADFLIIICLPFLMDNVVRWDWKFGDIPCRMLFMLAMNRQSGIIFLT 120
 Db 61 SSRIFLNLAVADFLIIICLPFLMDNVVRWDWKFGDIPCRMLFMLAMNRQSGIIFLT 120
 QY 121 VAVDRYFRVVRVPHHALKISNRTAAIISCLLWGTTIGLTVHLLKKKMPIONGANLCS 180
 Db 121 VAVDRYFRVVRVPHHALKISNRTAAIISCLLWGTTIGLTVHLLKKKMPIONGANLCS 180
 QY 181 SICTHTLQHEANFLLEFFFLGLIILFCS 208
 Db 181 SICTHTLQHEANFLLEFFFLGLIILFCS 208

RESULT 7
 GP81 MOUSE
 ID GP81 MOUSE STANDARD; PRT; 343 AA.
 AC Q8C131
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Probable G protein-coupled receptor GPR81.
 GN Name=Gpr81;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Daila E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Ferte G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 CC -!- FUNCTION: Orphan receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB083630; BAB89343.1; -.
DR EMBL; AB083055; BAC11806.2; -.
DR EMBL; BC063549; AA63549.1; -.
DR GO; GO:0050648; F:5-(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; NAS.
DR GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; NAS.
DR GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; NAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; NAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR GO; GO:0030817; P:regulation of cAMP biosynthesis; IDA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECSP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECSP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 423 AA; 45810 MW; 72ADA9F43A9EC051 CRC64;

Query Match 27.1%; Score 563; DB 2; Length 423;
Best Local Similarity 41.8%; Pred. No. 5.2e-31;
Matches 118; Conservative 52; Mismatches 88; Indels 24; Gaps 5;

QY 30 LPPVLGLERIFGLGNGLALWIFCFHLKSKSRIFLFLNLAVALDFLLIICLPFLMDNYVR 89
DB 95 LAPILALEFVLGLVGNLSALFICITRPWTSNTVFLSVLAADFLILSNLPURVDYLL 154
QY 90 RDWKEGDIPCRMLFMLAMNRQGSIFLTVVAVDRYFRVPHPHALNKISNRATAIISC 149
DB 155 HETWREGAAACKVNFMLSTNRTASVVFLLTAIALNRYLKVVQPHVLSRASVGAARVAG 214
QY 150 LMGITIGLTVHLLKKMPIONGANLCSFSFI-----CHTFQWHEAMFLEFPLGIL 205
DB 215 GLWVGILLNGHLL-----LSTFSGSCLSYRYGTRKPSASRHWQALYLEFPLALIL 269
QY 206 FCSARIISLRQRMORHAKIKRAITFIMVAIVFVICFLPSVVV---VRIREFWLLHTSG 262
DB 270 FAIVSGLTIRNGLGCGQAPQAMRVLANVAVYTCFLPSIFGWSWVAFWL----- 324
QY 263 TQNCVYRSVDLA---FFITLSTYMNMLDPVYVYFSSPSF 301
DB 325 ----SACRSIDLCTQLFHGSLAFTYLSVLDPLVLYCFSSPNF 362

RESULT 13
Q9NQ20 PRELIMINARY; PRT; 319 AA.
AC Q9NQ20;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BA517H2.2 (G protein-coupled receptor 31).
GN Name=GPR31;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Almeida J.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121935; CAB99329.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECSP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECSP_F1_2; 1.
KW Receptor.

SQ SEQUENCE 319 AA; 35074 MW; 2ACD0350AD7FB53A CRC64;
Query Match 23.9%; Score 496.5; DB 2; Length 319;
Best Local Similarity 36.4%; Pred. No. 1.5e-26;
Matches 110; Conservative 56; Mismatches 111; Indels 25; Gaps 5;

QY 33 VLGLERIFGLGNGLALWIFCFHLKSKSRIFLFLNLAVALDFLLIICLPFLMDNYVRWD 92
DB 20 LIGLECGELGNGVALWTFLFRVWKYAVYLLNLALADLLAACLPLPAAFYLSQA 79
QY 93 WKFGDIPCRMLFMLAMNRQGSIFLTVVAVDRYFRVPHPHALNKISNRATAIISC 152
DB 80 WHLGRVGCWALHFLDLSRSVGMFLAAVALDRYLRVHPRLKVNLLSPQAALGVSLVW 139
QY 153 GITIGLTVHLLKKMPIONGANLCSFSFICHTFQ-----WHEAMFLEFPLG 202
DB 140 LLMVALTCFGLLISEAQN-----TRCHSFYSRADGSGFSIIWQEALSCIQVLPFG 191
QY 203 IILFCSARIISL--RORQMDRHAKIKRAITFIMVAIVFVICFLPSVVVIRIFWLHT 260
DB 192 LIVFCNAGIIRALQKRLREPEKQPLQRAQALVTVVILFALCFPCFLARV----LMHI 247
QY 261 -SGTQNCVYRSVDLAFFITLSTYMNMLDPVYVYFSSPSFSTLINRCLQRMTG 319
DB 248 FQNLGSCRALCAVAHTSDVTGSLTYLSVLPVVCFSPTFRSSYRRVFHTLGRGQAA 307
QY 320 EP 321
DB 308 EP 309

RESULT 14
GP31_HUMAN STANDARD; PRT; 319 AA.
AC Q00270;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor GPR31.
GN Name=GPR31;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zingoni A., Rocchi M., Storlazzi C.T., Bernardini G., Santoni A.,
RA Napolitano M.;
RT "Isolation and chromosomal localization of GPR31, a human gene
RT encoding a putative G protein-coupled receptor."
RL Genomics 42:519-523(1997).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U65402; AAC51375.1; -.
CC Genew; HGNC:4486; GPR31.
CC MIM; 602043; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 16 Extracellular (Potential).
FT TRANSSEM 17 37 1 (Potential).
FT DOMAIN 38 52 Cytoplasmic (Potential).
FT TRANSSEM 53 73 2 (Potential).
FT DOMAIN 74 91 Extracellular (Potential).
FT TRANSSEM 92 110 3 (Potential).
FT DOMAIN 111 131 Cytoplasmic (Potential).
FT TRANSSEM 132 152 4 (Potential).
FT DOMAIN 153 180 Extracellular (Potential).
FT TRANSSEM 181 201 5 (Potential).
FT DOMAIN 202 219 Cytoplasmic (Potential).
FT TRANSSEM 220 240 6 (Potential).
FT DOMAIN 241 265 Extracellular (Potential).
FT TRANSSEM 266 284 7 (Potential).
FT DOMAIN 285 319 Cytoplasmic (Potential).
FT CARBOHYD 5 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 319 AA; 35079 MW; 7A4F164CD9C969DD CRC64;

Query Match 23.8%; Score 494.5; DB 1; Length 319;
Best Local Similarity 36.1%; Pred. No. 2.1e-26;
Matches 109; Conservative 57; Mismatches 111; Indels 25; Gaps 5;

Qy 33 VLGLFIFGLGNGLALWIFCFHLKSWKSSRIFFLNLAADVFLIIICLPFLMDNYVRRWD 92
Db 20 LLGLECGLLGNNAVALWTFIFRVVWKPYPVYLLNALADLLAACLFLAAYLSQA 79
Qy 93 WKFGDIPCRMLFMFLMANNROGSIIFLTVAVDYFRVYVPHHAKNKISNRTAAIISCLLW 152
Db 80 WHLGRVGCWALRFLLDLSRSVGMFLAVALDRLVYVPHLPRLKYNLLSPOAALGVSLVW 139
Qy 153 GITIGLTVHLLKKMPIONGGANLCSSFSICTHTQ-----WHEAMFLEFFLPLG 202
Db 140 LLMVLTCPGLLISEAQN-----TRCHSYRADSGFSIIWOEALSCQFVLPPG 191
Qy 203 ILFCSARIISLWLR--RQMDRHAKIKRAITFIMVVAIVFVICPLSPVVVIRIFWLLHT 260
Db 192 LIVFCNAGIIRALQKRLREPEKQFLQRAQALVTLVVVLFALCFPLCLARV---LMHI 247
Qy 261 -SGTQNCVRSVDLAFITLSFTYMNMSMLDPVYVYFSSPSFPNFFSTLINRCLQRKWTG 319
Db 248 FQNLGSCRALCAVAHSDVTGSLTYLHVSVPVYVYFSSPSPTFRSSRYRVRVHTLRGQAA 307
Qy 320 EP 321
Db 308 EP 309

RESULT 15
Q9JLS1 PRELIMINARY; PRT; 319 AA.
AC Q9JLS1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G protein coupled receptor.
GN Name=Tcp10c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431663; PubMed=10501965;
RA Schimenti J.C.;
RT "ORFless, intronless, and mutant transcription units in the mouse t
RL complex responder (Tcr) locus.";
DR Mamm. Genome 10:969-976(1999).
DR EMBL; AF140708; AAF26668.1; -.
DR MGD; MGI:98543; Tcp10c.
```

```
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 319 AA; 35551 MW; 571F6DFB485BD7C4 CRC64;

Query Match 23.1%; Score 481; DB 2; Length 319;
Best Local Similarity 35.7%; Pred. No. 1.8e-25;
Matches 109; Conservative 61; Mismatches 111; Indels 24; Gaps 7;

Qy 33 VLGLFIFGLGNGLALWIFCFHLKSWKSSRIFFLNLAADVFLIIICLPFLMDNYVRRWD 92
Db 20 MLTLECVLGLMGNAVALWTFIFRLKWKYPVAVYLVNLAADLLATSVPFAAFYLGKT 79
Qy 93 WKFGDIPCRMLFMFLMANNROGSIIFLTVAVDYFRVYVPHHAKNKISNRTAAIISCLLW 152
Db 80 WKLGHMPCQLLFLAFSCGVGVAFMLTVALDRLVYVPHLPRLKYNLLSLRAAGISSLIW 139
Qy 153 GITIGLTVHLLKKMPIONGGANLCSSF-----SICHTFQWHEAMFLEFFLPLGI 203
Db 140 LLMVLTCPQLLTCRTTON--STECPSFYPTGTGKAIATC-----QEVLFQVLLPFL 192
Qy 204 ILFCSARIISLWLR--QMDRHAKIKRAITFIMVVAIVFVICPLSPVVVIRIFWLLHT- 260
Db 193 ISFCNGLTTLQKRLSESKOPTIRARVLVAIMLLFGCLFPLSVLTV---LVHIF 248
Qy 261 SGTQNCVRSVDLAFITLSFTYMNMSMLDPVYVYFSSPSFPNFFSTLINRCLQRKWTG 320
Db 249 QEFKSCSVQQAIMRASDIAGSLTCLHSTLSPAIVCFSPNAPFTHSYRKVLKSLRGRRKAAE 308
Qy 321 -PDNN 324
Db 309 SPSDN 313

Search completed: October 20, 2005, 06:04:15
Job time : 61 secs
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Result No.	Score	Query Match	Length	DB	ID	Description	
1	2081	100.0	387	8	ADT08043	Human G-p	Adt08043
2	1996	95.9	387	5	AAU77992	Human inf	AAU77992
3	1996	95.9	387	5	AD63768	Human G p	Adf63768
4	1996	95.9	387	7	ADf28984	Human G p	Adf28984
5	1995	95.9	387	6	ADf48195	Human bla	Adf48195
6	1995	95.9	387	7	ADN38906	Cancer/an	Adn38906
7	1995	95.9	387	8	ADG60130	Human G-p	Adg60130
8	1995	95.9	625	7	ADf70463	Orphan re	Adf70463
9	1990	95.6	387	3	AAy90637	Human G p	Aay90637
10	1990	95.6	387	5	ABP54318	Human G p	Abp54318
11	1990	95.6	387	5	ABP598163	Human HM7	Abp598163
12	1990	95.6	387	5	AAU79041	Human G p	Aau79041
13	1990	95.6	387	6	ABP81898	Human G p	Abp81898
14	1990	95.6	387	7	ADQ22627	Human G p	Adq22627
15	1990	95.6	387	7	ADH14100	Human HM7	Adh14100
16	1990	95.6	387	7	ADf17891	Human HM7	Adf17891
17	1990	95.6	387	7	ADN38910	Cancer/an	Adn38910
18	1990	95.6	387	8	ADN011996	Human inf	Adn011996
19	1990	95.6	387	8	ADQ29488	Human' GFC	Ado29488
20	1990	95.6	387	8	ADQ59983	Human HM-	Ado59983
21	1990	95.6	387	8	ADQ32541	hrUP18 re	Ado32541
22	1990	95.6	387	8	ADR43757	Human HM7	Adr43757
23	1990	95.6	387	8	ADP23835	PRO polytp	Adp23835
24	1990	95.6	387	8	ADSI17050	Human 311	Adsi17050
25	1990	95.6	387	8	ADT08044	Human G-p	Adt08044

XX New nucleic acid molecules encoding HGRBM74 polypeptides of the G-
PT protein coupled receptor superfamily, useful for diagnosing, treating, or
PT ameliorating dyslipidaemia, diabetes, or inflammatory disorders.
XX
PS
XX Claim 5; Fig 1A-B; 332pp; English.
XX
CC The invention relates to an isolated human G-protein coupled receptor
CC (GPCR), HGRBM74 and encoding polynucleotides. The HGRBM74 polypeptide
CC can be expressed by standard recombinant methodology. The nucleic acid
CC molecules, polypeptides, modulators and methods are useful for
CC diagnosing, treating or ameliorating a pathological condition, e.g. a
CC disorder related to aberrant G-protein coupled signaling; a disorder
CC related to aberrant nicotinic acid dependent-G-protein coupled signaling;
CC a disorder related to aberrant cell cycle regulation; cardiovascular
CC disorders; an immune disorder; disorders associated with aberrant
CC nicotinic acid utilization; disorders associated with aberrant nicotinic
CC acid absorption; disorders associated with aberrant in nicotinic acid
CC responses; dyslipidaemia; diabetic dyslipidaemia; mixed dyslipidaemia;
CC hypercholesterolemia; hypertriglyceridemia; type II diabetes mellitus; type
CC I diabetes; insulin resistance; hyperlipidaemia; obesity; anorexia
CC nervosa; disease or disorders known to be associated with HM74; disease
CC or disorders known to be associated with HM74A; heart failure;
CC atherosclerosis; arteriosclerosis; hypertriglyceridemia; inflammatory
CC disorders; arthritis; rheumatoid arthritis; osteoarthritis; prosthetic
CC joint failure; gastrointestinal tract disorders; ulcerative colitis;
CC Crohn's disease; inflammatory bowel disorder; gastritis; mucosal
CC inflammation; enteropathy provoked by non-steroidal anti-inflammatory
CC drugs; lung disorders; adult respiratory distress syndrome; asthma;
CC cystic fibrosis; chronic obstructive pulmonary disease; myocardiitis;
CC multiple sclerosis; inflammation associated with diabetes mellitus;
CC glomerulonephritis; dermatitis; psoriasis; eczema; urticaria; burn injury
CC ; glaucoma; organ rejection; systemic lupus erythematosus; sepsis;
CC ischaemic heart disease; disorders associated with aberrant lipolysis;
CC stroke; dyslipidaemia; disorders associated with below average levels of
CC high density lipoprotein (HDL); disorders associated with above average
CC levels of very low density lipoprotein (VLDL); disorders associated with
CC above average levels of low density lipoprotein (LDL); and disorders
CC associated with above average levels of cholesterol. The present sequence
CC represents a human GPCR, HGRBM74.
XX
SQ Sequence 387 AA;

Query Match 100.0%; Score 2081; DB 8; Length 387;
Best Local Similarity 100.0%; Pred. No. 6.1e-207;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60
DB 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLIICLPFLMDNYYRRWDKFGDIPCRMLFMLAMNRQGSIIFLT 120
DB 61 SSRIFLNLAVADFLIICLPFLMDNYYRRWDKFGDIPCRMLFMLAMNRQGSIIFLT 120
QY 121 VAVDRFVVVPHHAIKNSRTAAIISCLLWGITITGLTVHLKXKQPTONGANICSSF 180
DB 121 VAVDRFVVVPHHAIKNSRTAAIISCLLWGITITGLTVHLKXKQPTONGANICSSF 180
QY 181 SICTTQWHEAMFLLFFPLGLIIFCSARIISLQRQMDRHAKIKRAITFTIMVAIVF 240
DB 181 SICTTQWHEAMFLLFFPLGLIIFCSARIISLQRQMDRHAKIKRAITFTIMVAIVF 240
QY 241 VICFLPSVVVRIIRIFWLLTSGTQNCVRSVDLAFITLSFTYMSMLDPVVYFSSPS 300
DB 241 VICFLPSVVVRIIRIFWLLTSGTQNCVRSVDLAFITLSFTYMSMLDPVVYFSSPS 300
QY 301 FPNFSTLINRCLOKWTGEPDNNRSTSVELTGDPNKTRCAPALMANSGEPSYILGP 360
DB 301 FPNFSTLINRCLOKWTGEPDNNRSTSVELTGDPNKTRCAPALMANSGEPSYILGP 360
QY 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387
DB 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387

DB 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387
RESULT 2
AAU77992
XX ID AAU77992 standard; protein; 387 AA.
XX AC AAU77992;
XX DT 02-JUL-2002 (first entry)
XX DE Human inflammation-associated GPCR EX20 polypeptide.
XX KW Human; inflammation-associated G-protein coupled receptor; GPCR; EX20;
XX KW inflammatory disease; asthma; adult respiratory distress syndrome; ARDS;
XX KW chronic obstructive pulmonary disease; COPD; bronchitis; emphysema;
XX KW pneumoconiosis; neutrophil; eosinophil related disorder; airway;
XX KW lung-related disorder; rheumatoid arthritis; inflammatory bowel disease;
XX KW ulcerative colitis; skin disease; eczematous dermatitis; receptor.
XX OS Homo sapiens.
XX WO200213845-A2.
XX PN 21-FEB-2002.
XX PD 16-AUG-2001; 2001WO-EP009466.
XX PF 18-AUG-2000; 2000US-00641653.
XX PR (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PI Jarai G, Yousefi S;
XX DR WPI: 2002-329542/36.
XX DR N-PSDB; ABK47759.
XX PT New pharmaceutical composition comprising EX20 polypeptide, EX20
PT polynucleotide, antibodies against EX20 polypeptide, antisense
PT oligonucleotides against EX20 polynucleotide, useful for treating
PT inflammatory disease.
XX PS Claim 2; Page 31-32; 36pp; English.
XX CC The present invention relates to human inflammation-associated G-protein
CC coupled receptor (GPCR) EX20 polypeptide and the polynucleotide sequence
CC encoding it. A pharmaceutical composition comprising EX20 polypeptide, a
CC variant of EX20, an antibody which immunoreacts with EX20, a
CC polynucleotide encoding EX20 or an antisense oligonucleotide comprising a
CC nucleotide sequence complementary to EX20 can be used in diagnostic and
CC therapeutic applications for treating an inflammatory disease. Such
CC inflammatory diseases include asthma, adult respiratory distress syndrome
CC (ARDS), chronic obstructive pulmonary disease (COPD) including chronic
CC bronchitis, emphysema, pneumoconiosis, neutrophil or eosinophil related
CC disorders, airway and lung-related disorders, rheumatoid arthritis, such as
CC eczematous dermatitis, ulcerative colitis, and skin diseases such as
CC -associated GPCR EX20 polypeptide
XX
SQ Sequence 387 AA;

Query Match 95.9%; Score 1996; DB 5; Length 387;
Best Local Similarity 96.1%; Pred. No. 4.1e-198;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60
DB 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLIICLPFLMDNYYRRWDKFGDIPCRMLFMLAMNRQGSIIFLT 120
DB 61 SSRIFLNLAVADFLIICLPFLMDNYYRRWDKFGDIPCRMLFMLAMNRQGSIIFLT 120

KW primary sclerosing cholangitis; Crohn's disease; antiinflammatory;
 KW antiasthmatic; receptor.
 XX OS Homo sapiens.
 XX US2003078218-A1.
 XX 24-APR-2003.
 XX 15-AUG-2001; 2001US-00930334.
 XX 15-AUG-2001; 2001US-00930334.
 XX (JARA/) JARAI G.
 XX (YOUS/) YOUSEFI S.
 XX Jarai G, Yousefi S;
 XX WPI; 2003-635083/60.
 XX N-PSDB; ADP28983.
 XX New pharmaceutical composition comprising a polypeptide, polynucleotide,
 PT antibody and/or antisense oligonucleotide, useful for diagnosing and/or
 PT treating an inflammatory and/or obstructive airways disease.
 XX Claim 1; SEQ ID NO 2; 18pp; English.
 XX The invention relates to a pharmaceutical composition comprising active
 CC ingredients of a human G protein-coupled receptor (GPCR) polypeptide, a
 CC polynucleotide encoding the polypeptide, an antibody which is
 CC immunoreactive with the polypeptide or an antisense oligonucleotide
 CC comprising a nucleotide sequence complementary to the polypeptide. The
 CC composition is used for treating an inflammatory disease or an
 CC obstructive airways disease, e.g. asthma, chronic obstructive pulmonary
 CC disease (COPD), respiratory tract inflammation, bronchitis, emphysema,
 CC adult respiratory distress syndrome (ARDS), rheumatoid arthritis,
 CC inflammatory bowel disease (IBD), ulcerative colitis, primary sclerosing
 CC cholangitis and Crohn's disease. The level of expression of the
 CC polynucleotide is used for diagnosing and monitoring inflammatory
 CC disease. The expression and/or activity of the polypeptide is also used
 CC for monitoring inflammatory disease and for screening of substrates
 CC useful for treating inflammatory disease. This sequence represents a
 CC human GPCR polypeptide, EX20.
 XX Sequence 387 AA;
 SQ
 Query Match 95.9%; Score 1996; DB 7; Length 387;
 Best Local Similarity 96.1%; Pred. No. 4.1e-198;
 Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MNRHHLDHFLEIDKKNCCVFRDDFTVKVLPVVLGLEFIFGLGNGLALWIFCFHLKSWK 60
 DB 1 MNRHHLDHFLEIDKKNCCVFRDDFTAKVLPVVLGLEFIFGLGNGLALWIFCFHLKSWK 60
 QY 61 SSRIFLNLAVADFLIICLPFLMDNVRRWDKFGDIPCRMLFMLAMNRQGSIIFLTV 120
 DB 61 SSRIFLNLAVADFLIICLPFLMDNVRRWDKFGDIPCRMLFMLAMNRQGSIIFLTV 120
 QY 121 VAVDRYFRVPHPHALNKNISNRATAIISCLLWGITTGLTVHLLKKKOMPIONGGANICSSF 180
 DB 121 VAVDRYFRVPHPHALNKNISNRATAIISCLLWGITTGLTVHLLKKKOMPIONGGANICSSF 180
 QY 181 SICTHFWHEAMFLEFFPLGLIILCSARIINSLRQQRQMDRHAKIKRAITFMVVAIYF 240
 DB 181 SICTHFWHEAMFLEFFPLGLIILCSARIINSLRQQRQMDRHAKIKRAITFMVVAIYF 240
 QY 241 VICFLPSVVVRIRIFWLLHTSGTQNCVEYRSVDLAFITLSFTYMSMLDPVVYYESSPS 300
 DB 241 VICFLPSVVVRIRIFWLLHTSGTQNCVEYRSVDLAFITLSFTYMSMLDPVVYYESSPS 300
 QY 301 FPNFFSTLINCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPSYLG 360
 DB 301 FPNFFSTLINCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPSYLG 360

QY 361 TSNHSHKKGCHQEPASLEKOLGCCIE 387
 DB 361 TSNHSHKKGCHQEPASLEKOLGCCIE 387
 RESULT 5
 ABR48195
 ID ABR48195 standard; protein; 387 AA.
 XX ABR48195;
 XX 12-JUN-2003 (first entry)
 XX Human bladder cancer associated protein sequence SEQ ID NO:108.
 XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
 XX Homo sapiens.
 XX WO2003003906-A2.
 XX 16-JAN-2003.
 XX 03-JUL-2002; 2002WO-US021338.
 XX 03-JUL-2001; 2001US-0302814P.
 XX 03-AUG-2001; 2001US-0310099P.
 XX 08-NOV-2001; 2001US-0343705P.
 XX 13-NOV-2001; 2001US-0350666P.
 XX 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Mack DH, Aziz N;
 XX WPI; 2003-201532/19.
 XX N-PSDB; ACC51008.
 XX Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX Claim 10; Page 269; 307pp; English.
 XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX Sequence 387 AA;
 SQ
 Query Match 95.9%; Score 1995; DB 6; Length 387;
 Best Local Similarity 96.1%; Pred. No. 5.2e-198;
 Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MNRHHLDHFLEIDKKNCCVFRDDFTVKVLPVVLGLEFIFGLGNGLALWIFCFHLKSWK 60
 DB 1 MNRHHLDHFLEIDKKNCCVFRDDFTAKVLPVVLGLEFIFGLGNGLALWIFCFHLKSWK 60
 QY 61 SSRIFLNLAVADFLIICLPFLMDNVRRWDKFGDIPCRMLFMLAMNRQGSIIFLTV 120
 DB 61 SSRIFLNLAVADFLIICLPFLMDNVRRWDKFGDIPCRMLFMLAMNRQGSIIFLTV 120

Db 61 SSRIFLNLAVALFLLIICLPVMDYVRRSDWKFGDIPCLVLFMFAMNRQGSIIIFLV 120
 Qy 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGTIGTLVHLLKKKMPIONGGANLCSF 180
 Db 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGTIGTLVHLLKKKLIQNGPANVCISF 180
 Qy 181 SICHTFOWHEAMFLLEFLPLGILFCSARIINSRLRQMDRHAHAKIKRAITFIMVAIVF 240
 Db 181 SICHTFOWHEAMFLLEFLPLGILFCSARIINSRLRQMDRHAHAKIKRAITFIMVAIVF 240
 Qy 241 VICPLPSVVVRIRIFWLLHSTGTQNCVYRSVDLAFFITLSFTYMNMLDPVVYFSSPS 300
 Db 241 VICPLPSVVVRIRIFWLLHSTGTQNCVYRSVDLAFFITLSFTYMNMLDPVVYFSSPS 300
 Qy 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPEALMANSGEPSYILGP 360
 Db 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPEALMANSGEPSYILGP 360
 Qy 361 TSNHSHKKGHCHQBPASLEKQLGCCIE 387
 Db 361 TSNHSHKKGHCHQBPASLEKQLGCCIE 387

RESULT 6

ADN38906

ID ADN38906 standard; protein; 387 AA.

XX AC

XX ADN38906;

XX DT 17-JUN-2004 (first entry)

XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:224.

XX KW Human; differential expression; cancer; angiogenic disorder;
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;
 KW detection; diagnosis; prognosis; drug screening; drug targeting;
 KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
 KW vulnery; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN W02003042661-A2.

XX PD 22-MAY-2003.

XX PF 13-NOV-2001; 2001US-0350666P.

XX PR 21-NOV-2001; 2001US-0332464P.

XX PR 29-NOV-2001; 2001US-0334393P.

XX PR 03-DEC-2001; 2001US-0335394P.

XX PR 14-DEC-2001; 2001US-0340376P.

XX PR 08-JAN-2002; 2002US-0347211P.

XX PR 10-JAN-2002; 2002US-0347349P.

XX PR 08-FEB-2002; 2002US-0355250P.

XX PR 13-FEB-2002; 2002US-0356714P.

XX PR 20-FEB-2002; 2002US-0359077P.

XX PR 04-MAR-2002; 2002US-0368809P.

XX PR 09-APR-2002; 2002US-0370110P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PR 05-JUN-2002; 2002US-0386614P.

XX PR 16-JUL-2002; 2002US-0396839P.

XX PR 22-JUL-2002; 2002US-0397775P.

XX PR 22-JUL-2002; 2002US-0397845P.

XX PR 09-SEP-2002; 2002US-0409450P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

XX PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX

DR WPI; 2003-458649/44.
 XX N-PSDB; ADN38905.

PT Determining the presence or absence of a pathological cell in a patient,
 useful for diagnosing, prognosing or treating cancer, comprises detecting
 a nucleic acid in a biological sample.

XX PS Claim 12; SEQ ID NO 224; 1385pp; English.

XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
 CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a polypeptide of the invention.

XX SQ Sequence 387 AA;

Query Match 95.9%; Score 1995; DB 7; Length 387;
 Best Local Similarity 96.1%; Pred. No. 5.2e-198;
 Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHELEIDKKNCCVFRDDFIKVLPPVLGLFIFGLGNGLALMIFCFHLKSWK 60
 Db 1 MNRHLLQDHELEIDKKNCCVFRDDFIKVLPPVLGLFIFGLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLNLAVALFLLIICLPVMDYVRRSDWKFGDIPCLVLFMFAMNRQGSIIIFLV 120
 Db 61 SSRIFLNLAVALFLLIICLPVMDYVRRSDWKFGDIPCLVLFMFAMNRQGSIIIFLV 120

Qy 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGTIGTLVHLLKKKMPIONGGANLCSF 180
 Db 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGTIGTLVHLLKKKLIQNGPANVCISF 180

Qy 181 SICHTFOWHEAMFLLEFLPLGILFCSARIINSRLRQMDRHAHAKIKRAITFIMVAIVF 240
 Db 181 SICHTFOWHEAMFLLEFLPLGILFCSARIINSRLRQMDRHAHAKIKRAITFIMVAIVF 240

Qy 241 VICPLPSVVVRIRIFWLLHSTGTQNCVYRSVDLAFFITLSFTYMNMLDPVVYFSSPS 300
 Db 241 VICPLPSVVVRIRIFWLLHSTGTQNCVYRSVDLAFFITLSFTYMNMLDPVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPEALMANSGEPSYILGP 360
 Db 301 FPNFFSTLINRCLQRKMTGPDNNRSTSVELTGPDKTRGAPEALMANSGEPSYILGP 360

Qy 361 TSNHSHKKGHCHQBPASLEKQLGCCIE 387
 Db 361 TSNHSHKKGHCHQBPASLEKQLGCCIE 387

RESULT 7

ADQ60130

ID ADQ60130 standard; protein; 387 AA.

XX AC

XX ADQ60130;

XX DT 07-OCT-2004 (first entry)

XX DE Human G-protein coupled receptor protein (GPCR) HM74 protein.

XX KW G-protein coupled receptor; GPCR ligand binding; N-formyl-L-methionine;

KW antiinflammatory; antiallergic; antirheumatic; antiarthritic;
 KW osteopathic; dermatological; immunosuppressive; immunodeficiency;
 KW allergy; rheumatism; osteoarthritis; lupus erythematosus; human; HM74;
 KW receptor.
 XX
 OS Homo sapiens.
 XX
 PN JP2004198202-A.
 XX
 PD 15-JUL-2004.
 XX
 PF 17-DEC-2002; 2002JP-00365684.
 XX
 PR 17-DEC-2002; 2002JP-00365684.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 2004-513647/49.
 XX
 DR N-PSDB; ADQ60131.
 XX
 XX Screening compound or its salt that affects binding of ligand of G-
 PT protein coupled receptor protein (HM74) with HM74, or its partial peptide
 PT or salt, by using N-formyl-L-methionine.
 XX
 PS Claim 1; SEQ ID NO 1; 51pp; Japanese.
 XX
 CC The invention relates to a novel method for screening a compound, or its
 CC salt, that affects the binding of the ligand of G-protein coupled
 CC receptor (GPCR) HM74, or its partial peptide or salt, by using
 CC N-formyl-L-methionine, where HM74 has a fully defined sequence as given
 CC in the specification. The method of the invention has antiinflammatory,
 CC antiallergic, antirheumatic, antiarthritic, osteopathic, dermatological,
 CC and immunosuppressive activities and may be useful for treating
 CC immunodeficiency disorders, such as allergy, rheumatism, osteoarthritis
 CC or lupus erythematosus. The current sequence is that of the human G-
 CC protein coupled receptor protein (GPCR) HM74 protein of the invention.
 XX
 SQ Sequence 387 AA;
 Query Match 95.9%; Score 1995; DB 8; Length 387;
 Best Local Similarity 96.1%; Pred. No. 5.2e-198;
 Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MNRHLLQDHFLEIDKKNCCVFRDDFTVKVLPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
 DB 1 MNRHLLQDHFLEIDKKNCCVFRDDFTAKVLPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
 QY 61 SSRIFLNLAVADFLIICLPFLMDNYVRRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120
 DB 61 SSRIFLNLAVADFLIICLPFLMDNYVRRSDWKFGDIPCLRLVLFMFAMNRQGSIIIFLTV 120
 QY 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITITGLTVHLLKKKMPIONGGANLCSSF 180
 DB 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITITGLTVHLLKKKLLQNGPANVCISF 180
 QY 181 SICTHFQWEAMFLLEFFPLGLGIILFCSARIISLQRQMDRHAHAKIKRAITFTIMVAIVF 240
 DB 181 SICTHFRWEAMFLLEFFPLGLGIILFCSARIISLQRQMDRHAHAKIKRAITFTIMVAIVF 240
 QY 241 VICFLPSVVVRIRIFWLLHTSGTQNCCEVRSVDLAFITILSFTYMNMSMLDPVVYYFSSPS 300
 DB 241 VICFLPSVVVRIRIFWLLHTSGTQNCCEVRSVDLAFITILSFTYMNMSMLDPVVYYFSSPS 300
 QY 301 FPNFSTLNRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPSVYLGP 360
 DB 301 FPNFSTLNRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPSVYLGP 360
 QY 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387
 DB 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387

RESULT 8

ADF70463
 ID ADF70463 standard; protein; 625 AA.
 XX
 AC ADF70463;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Orphan receptor ligand-related human protein SeqID86.
 XX
 KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
 KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
 KW GFPuv; Enhanced GFP; EGFP; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003071272-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 21-FEB-2003; 2003WO-JP001901.
 XX
 PR 22-FEB-2002; 2002JP-00045728.
 XX
 PR 23-JUL-2002; 2002JP-00213949.
 PR 11-OCT-2002; 2002JP-00298237.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
 XX
 DR WPI; 2003-697654/66.
 XX
 DR N-PSDB; ADF70565.
 XX
 PT Transformation of cells with a fusion protein of an orphan receptor
 PT protein with a fluorescent protein useful for identification of ligands
 PT to the orphan receptor.
 XX
 PS Disclosure; SEQ ID NO 86; 594pp; Japanese.
 XX
 CC This invention relates to a novel method of identifying ligands to an
 CC orphan receptor protein which comprises transforming cells with DNA
 CC encoding a fusion protein of the orphan receptor with a fluorescent
 CC protein, so that the fusion protein is expressed in the cells (or cell
 CC membranes isolated from them) and contacting the cells with the potential
 CC ligand to be tested. A suitable fluorescent protein for incorporation in
 CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
 CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
 CC identification of ligands binding to an orphan receptor protein.
 XX
 SQ Sequence 625 AA;
 Query Match 95.9%; Score 1995; DB 7; Length 625;
 Best Local Similarity 96.1%; Pred. No. 9.8e-198;
 Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MNRHLLQDHFLEIDKKNCCVFRDDFTVKVLPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
 DB 1 MNRHLLQDHFLEIDKKNCCVFRDDFTAKVLPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
 QY 61 SSRIFLNLAVADFLIICLPFLMDNYVRRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120
 DB 61 SSRIFLNLAVADFLIICLPFLMDNYVRRSDWKFGDIPCLRLVLFMFAMNRQGSIIIFLTV 120
 QY 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITITGLTVHLLKKKMPIONGGANLCSSF 180
 DB 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITITGLTVHLLKKKLLQNGPANVCISF 180
 QY 181 SICTHFQWEAMFLLEFFPLGLGIILFCSARIISLQRQMDRHAHAKIKRAITFTIMVAIVF 240
 DB 181 SICTHFRWEAMFLLEFFPLGLGIILFCSARIISLQRQMDRHAHAKIKRAITFTIMVAIVF 240
 QY 241 VICFLPSVVVRIRIFWLLHTSGTQNCCEVRSVDLAFITILSFTYMNMSMLDPVVYYFSSPS 300
 DB 241 VICFLPSVVVRIRIFWLLHTSGTQNCCEVRSVDLAFITILSFTYMNMSMLDPVVYYFSSPS 300

QY 301 FPNFSTLINRCLQKMTGEPDNNRSTSVLTGDPNKTGAPALMANSGEPSYLG 360
 DB 301 FPNFSTLINRCLQKMTGEPDNNRSTSVLTGDPNKTGAPALMANSGEPSYLG 360
 QY 361 TSNNHKKGHCHQBPASLEKOLGCCIE 387
 DB 361 TSNNHKKGHCHQBPASLEKOLGCCIE 387

RESULT 9
 AAY90637
 ID AAY90637 standard; protein; 387 AA.
 AC AAY90637;
 XX
 XX 21-AUG-2000 (first entry)
 DT
 DE Human G protein-coupled receptor HM74.
 XX
 KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
 KW antagonist.
 XX
 OS Homo sapiens.
 XX
 XX WO200022129-A1.
 XX
 XX 20-APR-2000.
 XX
 PF 12-OCT-1999; 99WO-US023938.
 XX
 XX 13-OCT-1998; 98US-00170496.
 XX
 XX (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Chalmers DT, Liaw CW;
 XX
 XX WPI; 2000-329165/28.
 DR N-PSDB; AAA30658.
 XX
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents.
 XX
 PS Example 1; Page 185-187; 341pp; English.
 XX
 CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
 CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
 CC and AAA30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
 CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present sequence
 CC represents a human wild-type GPCR referred to in an exemplification of
 CC the invention
 XX
 XX Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 3; Length 387;
 Best Local Similarity 95.9%; Pred. No. 1.7e-197;
 Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLODHELEIDKKNCCVFRDDPIVKVLPVGLGFIKGLGNGLALMIFCFHLKSWK 60
 DB 1 MNRHHLODHELEIDKKNCCVFRDDPIAKVLPVGLGFIKGLGNGLALMIFCFHLKSWK 60
 QY 61 SSRIFLNLAVADFLIICLPFLMDNYYVRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120
 DB 61 SSRIFLNLAVADFLIICLPFVMDYYVRSDNFGDIPCLRLVLFMAMNRQGSIIIFLTV 120
 QY 121 VAVDRFVRVPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSF 180
 DB 121 VAVDRFVRVPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKLLIQNGPANVCISF 180
 QY 181 SICTFOWHEAMFLLEFFLPLGILFCSARIISLRODMRHAHAKIKRAITFINMVAIVF 240
 DB 181 SICTFOWHEAMFLLEFFLPLGILFCSARIISLRODMRHAHAKIKRAITFINMVAIVF 240
 QY 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVLAFFITLSFTYMNMLDPVVVYFSSPS 300
 DB 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVLAFFITLSFTYMNMLDPVVVYFSSPS 300
 QY 301 FPNFSTLINRCLQKMTGEPDNNRSTSVLTGDPNKTGAPALMANSGEPSYLG 360
 DB 301 FPNFSTLINRCLQKMTGEPDNNRSTSVLTGDPNKTGAPALMANSGEPSYLG 360
 QY 361 TSNNHKKGHCHQBPASLEKOLGCCIE 387
 DB 361 TSNNHKKGHCHQBPASLEKOLGCCIE 387

RESULT 10
 ABP54318
 ID ABP54318 standard; protein; 387 AA.
 XX
 XX ABP54318;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Human G protein coupled receptor HM74 protein SEQ ID NO:8.
 XX
 KW Human; G protein coupled receptor; GPCR; HGPBMY27; antiinflammatory;
 KW antiinfectivity; pulmonary; cytostatic; nephrotropic; hormonal;
 KW circulatory; gene therapy; inflammatory disorder; reproductive disorder;
 KW pulmonary disorder; cancer; renal disorder; connective tissue disorder;
 KW endocrine disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200272755-A2.
 PN
 PD 19-SEP-2002.
 XX
 XX 06-MAR-2002; 2002WO-US006796.
 PF
 XX 07-MAR-2001; 2001US-0273808P.
 PR
 XX 27-MAR-2001; 2001US-0278983P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Ramanathan C, Feder J, Mintier G, Cacace A, Barber L;
 XX WPI; 2002-657945/70.
 DR
 XX New polynucleotide encoding a human G-protein coupled receptor for
 PT preventing, treating, or ameliorating e.g. an inflammatory, reproductive,
 PT pulmonary, renal connective tissue, or endocrine disorder.
 XX
 PS Disclosure; Fig 2A-B; 356pp; English.
 XX
 CC The present invention describes a human G protein coupled receptor

(GPCR), designated HGRBMY27 (I). (I) has antiinflammatory, antiinfertility, pulmonary, cytostatic, nephrotropic, hormonal and circulatory activities, and can be used in gene therapy. (I) or the protein encoded by it can be used to prevent, treat, or ameliorate a medical condition, such as inflammatory disorders, reproductive disorders, pulmonary disorders, cancer, renal disorders, connective tissue disorders, endocrine disorders, or disorders involving aberrations in tubular tissues. They can also be used to diagnose a pathological condition or a susceptibility to (I). The protein can be used to screen for candidate compounds capable of modulating activity of a GPCR polypeptide. The present sequence represents a GPCR given in comparison with the HGRBMY27 protein in the exemplification of the present invention

XX
SQ Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 5; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.7e-197;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLDHFLFLEIDKKNCVFRDDFIKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
Db 1 MNRHHLDHFLFLEIDKKNCVFRDDFIKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLLIICLPFLMDNYVRWDMKFGDIPCLRLMFLMNMNRQSGIIFLTV 120
Db 61 SSRIFLNLAVADFLLIICLPFLMDNYVRWDMKFGDIPCLRLMFLMNMNRQSGIIFLTV 120

QY 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIONGGANICSSF 180
Db 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIONGGANICSSF 180

QY 181 SICTHTQWHEAMFLEFFPLGLIIFCSARIISLQRQMDRAKIKRAITFTMVVAIVF 240
Db 181 SICTHTQWHEAMFLEFFPLGLIIFCSARIISLQRQMDRAKIKRAITFTMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVIYFSSPS 300
Db 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVIYFSSPS 300

QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
Db 301 FPNFFSTLINRCLQRKWTGEPDNNRSTVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360

QY 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387
Db 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387

RESULT 11
ABB98163
ID ABB98163 standard; protein; 387 AA.
XX
AC ABB98163;
DT
XX 05-NOV-2002 (first entry)
DE Human HM74-like GPCR protein #2.
XX
KW Human; HM74-like G protein coupled receptor; GPCR; antibacterial; fungicide; viricide; protozoacide; analgesic; cytostatic; antiaschmatic; hypertensive; hypotensive; antianginal; cardiant; osteopathic; anorectic; antiulcer; anti allergic; antiinflammatory; neuroprotective; neuroleptic; antiparkinsonian; anticonvulsant; nootropic; tranquiliser; antimanic; antidepressant; antidiabetic; cerebroprotective; antiarthritic; antiilepessant; gynecological; depilatory; immunomodulator; bacterial; fungal; protozoan; viral; infection; human immunodeficiency virus; cancer; anorexia; asthma; central nervous system disease; cardiovascular disease; hypotension; hypertension; urinary retention; osteoporosis; obesity; ulcer; inflammation; allergy; multiple sclerosis; neurological disorder; dyskinesia; Parkinson's disease; manic depression; dementia; obesity; wasting disorder; stroke; osteoarthritis; respiratory; type 2 diabetes; thrombolic disease; reduced fertility; pregnancy;

menstrual irregularities; hirsutism; stress incontinence; gene therapy.

XX
OS Homo sapiens.
XX WO200194385-A2.
XX 13-DEC-2001.
XX 05-JUN-2001; 2001WO-EP006380.
XX 05-JUN-2000; 2000US-0208912P.
XX (FARB) BAYER AG.
XX
XX Ramakrishnan S;
XX WPI; 2002-566439/60.
XX
XX New human HM74-like G-protein coupled receptor polypeptide and polynucleotide, useful for treating cancer, cardiovascular disease, psychotic and neurological disorders, asthma, obesity and inflammation.

PT
PT
PT
XX
PS Disclosure; Fig 4; 105pp; English.

XX
XX The invention relates to an isolated HM74-like G-protein coupled receptor (GPCR) polypeptide. Polypeptides and polynucleotides of the invention are useful for screening for agents which decrease the activity of HM74-like GPCR polypeptides. Compositions of the invention are useful for modulating the activity of HM74-like GPCR in a disease including bacterial, fungal, protozoan and viral infection, particularly human immunodeficiency viruses, cancer, anorexia, asthma, central nervous system disease, cardiovascular disease, hypotension, hypertension, urinary retention, osteoporosis, obesity, ulcer, inflammation, allergy, multiple sclerosis, neurological disorder and dyskinesias such as Parkinson's disease, manic depression, and dementia. The HM74-like GPCR gene or its portion or product are useful for treating obesity, wasting disorders, stroke, osteoarthritis, respiratory problems, type 2 diabetes, thrombolic disease, reduced fertility, complications of pregnancy, menstrual irregularities, hirsutism and stress incontinence. Polypeptides and polynucleotides of the invention may also be used in gene therapy. The current sequence represents a human HM74-like GPCR protein

XX
SQ Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 5; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.7e-197;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLDHFLFLEIDKKNCVFRDDFIKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
Db 1 MNRHHLDHFLFLEIDKKNCVFRDDFIKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLLIICLPFLMDNYVRWDMKFGDIPCLRLMFLMNMNRQSGIIFLTV 120
Db 61 SSRIFLNLAVADFLLIICLPFLMDNYVRWDMKFGDIPCLRLMFLMNMNRQSGIIFLTV 120

QY 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIONGGANICSSF 180
Db 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIONGGANICSSF 180

QY 181 SICTHTQWHEAMFLEFFPLGLIIFCSARIISLQRQMDRAKIKRAITFTMVVAIVF 240
Db 181 SICTHTQWHEAMFLEFFPLGLIIFCSARIISLQRQMDRAKIKRAITFTMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVIYFSSPS 300
Db 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVIYFSSPS 300

QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
Db 301 FPNFFSTLINRCLQRKWTGEPDNNRSTVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360

QY 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387

Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	1	MNRHLLQDHFLEIDKKNCCVFRDDFI	VKVLPPVVLGLGFI	GLGLGGLALMIFCFHLKSWK	60						
Db	1	MNRHLLQDHFLEIDKKNCCVFRDDFI	AKVLPVVLGLGFI	GLGLGGLALMIFCFHLKSWK	60	QY	61	SSRIFENLAVADFLIIICLP	PELMDNVYRWDKFGDI	PCRLMFLMAMNQSGIIFLTV	120				
Db	61	SSRIFENLAVADFLIIICLP	PELMDNVYRWDKFGDI	PCRLMFLMAMNQSGIIFLTV	120	Db	61	SSRIFENLAVADFLIIICLP	PFVMDYVRRSDWNF	GDI	PCRLVLFMFAMNQSGIIFLTV	120			
QY	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	180		
Db	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	180		
QY	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240	QY	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240
Db	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240	Db	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240
QY	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300	QY	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300
Db	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300	Db	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300
QY	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360	QY	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360
Db	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360	Db	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360
QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387
Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387
RESULT 13															
ABP81898															
ID	ABP81898 standard; protein; 387 AA.														
XX															
AC	ABP81898;														
XX															
DT	04-MAR-2003 (first entry)														
XX															
DE	Human G protein-coupled receptor HM74 protein SEQ ID NO:281.														
DE															
XX	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;														
KW	G protein-coupled receptor modulator; antibody; immune-related disease;														
KW	growth-related disease; cell regeneration-related disease; AIDS; cancer;														
KW	immunological-related cell proliferative disease; autoimmune disease;														
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;														
KW	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;														
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; pain;														
KW	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;														
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;														
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;														
XX	ulcer.														
XX															
OS	Homo sapiens.														
XX															
PN	WO200261087-A2.														
XX															
PD	08-AUG-2002.														
XX															
PF	19-DEC-2001; 2001WO-US050107.														
XX															
PR	19-DEC-2000; 2000US-0257144P.														
XX															
PA	(LIFE-) LIFESPAN BIOSCIENCES INC.														
XX															
PI	Burner GC, Roush CL, Brown JP;														
XX															
DR	WPI; 2003-046718/04.														
XX															
DR	N-PSDB; ABZ42745.														
XX															
PT	New isolated antigenic peptides e.g., for G protein-coupled receptors														
PT	(GPCR), useful for diagnosing and designing drugs for treating conditions														
PT	in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or														
XX	autoimmune diseases.														

Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	1	MNRHLLQDHFLEIDKKNCCVFRDDFI	VKVLPPVVLGLGFI	GLGLGGLALMIFCFHLKSWK	60						
Db	1	MNRHLLQDHFLEIDKKNCCVFRDDFI	AKVLPVVLGLGFI	GLGLGGLALMIFCFHLKSWK	60	QY	61	SSRIFENLAVADFLIIICLP	PELMDNVYRWDKFGDI	PCRLMFLMAMNQSGIIFLTV	120				
Db	61	SSRIFENLAVADFLIIICLP	PELMDNVYRWDKFGDI	PCRLMFLMAMNQSGIIFLTV	120	Db	61	SSRIFENLAVADFLIIICLP	PFVMDYVRRSDWNF	GDI	PCRLVLFMFAMNQSGIIFLTV	120			
QY	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	180		
Db	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	121	VAVDRYFRVPHHALNKISNR	TAAIISCLLWG	ITIGLTVHLLKKKMP	IQNGGANLCS	SS	180		
QY	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240	QY	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240
Db	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240	Db	181	SICHTFOWHEAMLEFFL	PLGILFCSARIISL	RORQMDRHA	KIKRAITFI	MVAIVF	240
QY	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300	QY	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300
Db	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300	Db	241	VICFLPSVVVRI	RIFWLLHSTG	QNCVRSVDL	AFITISFTY	MNSMLDPVYFSSPS	300
QY	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360	QY	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360
Db	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360	Db	301	FPNFFSTLINRCLQR	KMTGPDNNRST	SVELTGD	PNKTRGAPEAL	MANSGEPS	360
QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	QY	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387
Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387	Db	361	TSNNHKKGGHCHQBPASLEKQLGCCIE	387
RESULT 13															
ABP81898															
ID	ABP81898 standard; protein; 387 AA.														
XX															
AC	ABP81898;														
XX															
DT	04-MAR-2003 (first entry)														
XX															
DE	Human G protein-coupled receptor HM74 protein SEQ ID NO:281.														
DE															
XX	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;														
KW	G protein-coupled receptor modulator; antibody; immune-related disease;														
KW	growth-related disease; cell regeneration-related disease; AIDS; cancer;														
KW	immunological-related cell proliferative disease; autoimmune disease;														
KW	Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;														
KW	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;														
KW	graft versus host disease; Parkinson's disease; multiple sclerosis; pain;														
KW	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;														
KW	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;														
KW	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;														
XX	ulcer.														
XX															
OS	Homo sapiens.														
XX															
PN	WO200218938-A1.														
XX															
PD	07-MAR-2002.														
XX															
PF	23-AUG-2001; 2001WO-BF009727.														
XX															
PR	01-SEP-2000; 2000GB-00021484.														
XX															
PA	(BOEH) BOEHRINGER INGELHEIM PHARMA KG.														
XX															
PI	Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K;														
PI	Weith A;														
WPI	2002-315590/35.														
DR	N-PSDB; ABK48114.														
XX															
PT	Determining an expression level of ILM (a macrophage surface receptor),														
PT	for the diagnosis or monitoring of chronic inflammatory airway disease,														
PT	comprises determining the level of the ILM receptor expressed in a														
PT	macrophage.														
XX															
XX	Claim 7; Page 72-74; 79pp; English.														
XX															
CC	The invention relates to determining an expression level of an ILM														
CC	receptor (macrophage surface receptor), comprises determining the level														
CC	of an ILM receptor expressed in a macrophage. Also included are a method														
CC	of determining whether a substance is an activator or an inhibitor of an														
CC	ILM receptor, involving applying the substance to a test system which														
CC	generates a measurable read-out upon modulation of the ILM receptor or an														
CC	ILM receptor function, a test system for determining whether a substance														
CC	is an activator or an inhibitor of an ILM receptor function,														
CC	characterised in that the receptor is involved in a chronic inflammatory														
CC	airway disease and where the receptor plays a role in mediating														
CC	inflammation comprising: (i) an ILM receptor; (ii) an expression vector														
CC	capable of expressing an ILM receptor in a cell; or (iii) a host cell														
CC	transformed with an expression vector capable of expressing the ILM														
CC	receptor and a substance determined to be an activator or inhibitor of an														
CC	ILM receptor. The methods are useful for the diagnosis or monitoring of a														
CC	chronic inflammatory airway disease, e.g. chronic bronchitis and chronic														
CC	obstructive pulmonary disease (COPD). The substance determined to be an														
CC	activator or inhibitor of an ILM receptor, is useful for treating the														
CC	diseases and for modulating an ILM receptor in a macrophage. The present														
CC	sequence is an ILM receptor which is differentially expressed and which														
CC	is involved in causing the induction and/or maintenance of the														
CC	hyperactive status of macrophages involved in an inflammatory process														
XX															
XX	Sequence 387 AA;														

Query Match	95.6%;	Score	1990;	DB	5;	Length	387;
Best Local Similarity	95.9%;	Pred.	No. 1.7e-197;				
Matches	371;	Conservative	6;	Mismatches	10;	Indels	0;
						Gaps	0;

DB 361 TSNNHKKGHCHQBPASLEKQLGCCIE 387

RESULT 12

AAU79041 standard; protein; 387 AA.

AAU79041;

18-JUN-2002 (first entry)

Human G protein-coupled receptor, HM74 receptor.

Human; G protein-coupled; receptor; HM74; ILM receptor; macrophage surface receptor; antiinflammatory; pulmonary; chronic inflammatory airway disease; chronic bronchitis; chronic obstructive pulmonary disease; COPD.

Homo sapiens.

WO200218938-A1.

07-MAR-2002.

23-AUG-2001; 2001WO-EP009727.

01-SEP-2000; 2000GB-00021484.

(BOEH) BOEHRINGER INGELHEIM PHARMA KG.

Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K; Weith A;

WPI; 2002-315580/35.

N-PSDB; ABK48114.

Determining an expression level of ILM (a macrophage surface receptor), for the diagnosis or monitoring of chronic inflammatory airway disease, comprises determining the level of the ILM receptor expressed in a macrophage.

Claim 7; Page 72-74; 79pp; English.

The invention relates to determining an expression level of an ILM receptor (macrophage surface receptor), comprises determining the level of an ILM receptor expressed in a macrophage. Also included are a method of determining whether a substance is an activator or an inhibitor of an ILM receptor, involving applying the substance to a test system which generates a measurable read-out upon modulation of the ILM receptor or an ILM receptor function, a test system for determining whether a substance is an activator or an inhibitor of an ILM receptor function, characterized in that the receptor is involved in a chronic inflammatory airway disease and where the receptor plays a role in mediating inflammation comprising: (i) an ILM receptor; (ii) an expression vector capable of expressing an ILM receptor in a cell; or (iii) a host cell transformed with an expression vector capable of expressing the ILM receptor and a substance determined to be an activator or inhibitor of an ILM receptor. The methods are useful for the diagnosis or monitoring of a chronic inflammatory airway disease, e.g. chronic bronchitis and chronic obstructive pulmonary disease (COPD). The substance determined to be an activator or inhibitor of an ILM receptor, is useful for treating the diseases and for modulating an ILM receptor in a macrophage. The present sequence is an ILM receptor which is differentially expressed and which is involved in causing the induction and/or maintenance of the hyperactive status of macrophages involved in an inflammatory process

Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 5; Length 387; Best Local Similarity 95.9%; Pred. No. 1.7e-197; Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)

CC any one of 1601 sequences (see ABP2019 to ABP83619) of 12-24 amino

CC acids. Also described: (1) an assay for the detection of a particular G

CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

CC and (2) an isolated antibody having high specificity and high affinity or

CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in

CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an

CC antibody against a particular GPCR, and in the production of specific

CC antibodies. The peptides and antibodies are also useful for detecting the

CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell

CC regeneration-related disease, immunological-related cell proliferative

CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

CC atherosclerosis, bacterial, fungal, protozoan or viral infections,

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host

CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, memory

CC anxiety, depression, schizophrenia, dementia, mental retardation, memory

CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be

CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode

CC GPCR proteins given in ABP1675 to ABP2018, which are used in the

CC exemplification of the present invention

XX

SQ Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 6; Length 387;

Best Local Similarity 95.9%; Pred. No. 1.7e-197;

Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60

DB 1 MNRHLLQDHFLEIDKKNCCVFRDDFIAKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLIIICLPFLMDNYVRRWDKFGDIPCRMLFMLAMNRQSGIIFLTV 120

DB 61 SSRIFLNLAVADFLIIICLPFLMDNYVRRWDKFGDIPCRMLFMLAMNRQSGIIFLTV 120

QY 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGITITGLTVHLLKKXMPIONGANLCSSF 180

DB 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGITITGLTVHLLKKXLLQNGPANVCISF 180

QY 181 SICTTQWHEAMFLEFFLPLGLIIFCSARIISLQRQMDRHAQIKRAITFTIMVVAIVF 240

DB 181 SICTTFRWHEAMFLEFFLPLGLIIFCSARIISLQRQMDRHAQIKRAITFTIMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300

DB 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300

QY 301 FPNFFSTLNRCLQRKMTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPSPSYLGP 360

DB 301 FPNFFSTLNRCLQRKMTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPSPSYLGP 360

QY 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387

DB 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387

RESULT 14

ADC22627

ID ADC22627 standard; protein; 387 AA.

XX

AC ADC22627;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human G protein-coupled receptor (GPCR) polypeptide #29.

XX

KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;

KW intracellular-3 region; IC3; receptor.

XX Homo sapiens.

OS

PN US6553339-B1.

XX

XX 29-APR-2003.

PD

XX 13-OCT-1998; 98US-00170496.

FF

XX 14-APR-1997; 97US-00839449.

PR

XX 14-APR-1998; 98US-00060188.

PR

XX 26-JUN-1998; 98US-0090783P.

PR

XX 07-AUG-1998; 98US-0095677P.

PR

XX (AREN-) ARENA PHARM INC.

PA

XX Liaw CW, Behan DP, Chalmers DT;

PI

XX WPI; 2003-742861/70.

DR

XX N-PSDB; ADC22626.

DR

XX

XX Creating a constitutively active version of an endogenous human G protein

PT coupled receptor (GPCR) comprises substituting a specific amino acid in

PT the transmembrane-6 region with a different amino acid, and testing for

PT constitutive activity.

PT

XX

XX Example 1; SEQ ID NO 108; 221pp; English.

PS

XX The invention relates to a method for treating a non-endogenous,

CC constitutively active version of an endogenous human G protein-coupled

CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an

CC intracellular-3 (IC3) region, by substituting a specific amino acid in

CC the TM6 region with a different amino acid, and testing for constitutive

CC activity. The method is useful for creating a constitutively active

CC version of an endogenous human GPCR that comprises a transmembrane 6

CC region and an intracellular loop 3 region. The altered human GPCR

CC polypeptides are useful for screening test compounds for identification

CC of inverse agonists or partial agonists of GPCR polypeptides, which may

CC have therapeutic uses. The altered GPCRs may also be used in vivo or in

CC vitro in biological research. A nucleic acid encoding the altered GPCR

CC may be used to create a transgenic animal expressing the altered GPCR.

CC The method allows screening for compounds that modulate the activity of a

CC human G protein-coupled receptor without the need for provision of a

CC ligand for the receptor. This is particularly useful in allowing

CC screening of compounds against orphan receptors for which no ligand is

CC currently known. This sequence represents a human GPCR polypeptide of the

CC invention.

CC

XX

SQ Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 7; Length 387;

Best Local Similarity 95.9%; Pred. No. 1.7e-197;

Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60

DB 1 MNRHLLQDHFLEIDKKNCCVFRDDFIAKVLPPVGLGFIPLGLNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLIIICLPFLMDNYVRRWDKFGDIPCRMLFMLAMNRQSGIIFLTV 120

DB 61 SSRIFLNLAVADFLIIICLPFLMDNYVRRWDKFGDIPCRMLFMLAMNRQSGIIFLTV 120

QY 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGITITGLTVHLLKKXMPIONGANLCSSF 180

DB 121 VAVDRYFRVPHHALNKISNRTAAIISCLLWGITITGLTVHLLKKXLLQNGPANVCISF 180

QY 181 SICTTQWHEAMFLEFFLPLGLIIFCSARIISLQRQMDRHAQIKRAITFTIMVVAIVF 240

DB 181 SICTTFRWHEAMFLEFFLPLGLIIFCSARIISLQRQMDRHAQIKRAITFTIMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300

Db 241 VICFLPSVVVRIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMSMLDVPVYFSSPS 300
Qy 301 FPNFFSTLINCLQKMTGEPDNNRSTSVELTGPDKTRGAPEALMANSGEPMSPSYLGP 360
Db 301 FPNFFSTLINCLQKMTGEPDNNRSTSVELTGPDKTRGAPEALMANSGEPMSPSYLGP 360
Qy 361 TSNHNSKKGHCHQBPASLEKOLGCCIE 387
Db 361 TSNHNSKKGHCHQBPASLEKOLGCCIE 387

RESULT 15
ADH14100
ID ADH14100 standard; protein; 387 AA.
AC ADH14100;
XX
XX
DT 11-MAR-2004 (first entry)
XX Human HM74.
XX
XX human; non-endogenous; G protein-coupled receptor; GPCR; receptor.
XX Homo sapiens.
OS
XX
XX US2003105292-A1.
XX
XX 05-JUN-2003.
XX
XX 20-SEP-2002; 2002US-00251385.
XX
XX 26-JUN-1998; 98US-0090783P.
PR 07-AUG-1998; 98US-0095677P.
PR 13-OCT-1998; 98US-00170496.
XX
XX (LIAW/) LIAW C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
XX
XX Liaw CW, Behan DP, Chalmers DT;
XX
XX WPI; 2003-801247/75.
DR N-PSDB; ADH14099.
XX

New constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor for the identification of therapeutic compounds, such as agonists.

Example 1; SEQ ID NO 108; 227pp; English.

The invention relates to a constitutively active, non-endogenous version of an endogenous human G protein-coupled receptor (GPCR). The GPCR is used for screening therapeutic compounds as inverse agonists, agonists or partial agonists. The GPCR can be also be used to elucidate and understand the roles of GPCRs in normal and diseased humans. The GPCR need not be purified and isolated to be used to screen for therapeutic compounds. The utility of the GPCR as a research tool is enhanced because the role of a particular receptor can be understood before the endogenous ligand is identified. The present sequence is used in the exemplification of the present invention.

Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 7; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.7e-197;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MNRHLLQDHFLEIDKNCVFRDDFIVKVLPPVLGLBFIQGLGNGLMIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKNCVFRDDFIAKVLPPVLGLBFIQGLGNGLMIFCFHLKSWK 60
Qy 61 SSRIFLNLAVADFLLIICLPFYMDYVRRSDWNFGDIPCKRLVLFMFAMNRQGSIIFLT 120

Db 61 SSRIFLNLAVADFLLIICLPFYMDYVRRSDWNFGDIPCKRLVLFMFAMNRQGSIIFLT 120
Qy 121 VAVDRYFRVPHPHALNKISNRATAAIIISCLLWGITIGLTVHLLKKKWPIONGGANLCSF 180
Db 121 VAVDRYFRVPHPHALNKISNRATAAIIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180
Qy 181 SICTFOWHEAMFLLEFFPLGIIILFCSARIINSLRQRMDRHAKIKRAITFIWVAIVF 240
Db 181 SICTFRWHEAMFLLEFFPLGIIILFCSARIINSLRQRMDRHAKIKRAITFIWVAIVF 240
Qy 241 VICFLPSVVVRIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMSMLDVPVYFSSPS 300
Db 241 VICFLPSVVVRIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMSMLDVPVYFSSPS 300
Qy 301 FPNFFSTLINCLQKMTGEPDNNRSTSVELTGPDKTRGAPEALMANSGEPMSPSYLGP 360
Db 301 FPNFFSTLINCLQKMTGEPDNNRSTSVELTGPDKTRGAPEALMANSGEPMSPSYLGP 360
Qy 361 TSNHNSKKGHCHQBPASLEKOLGCCIE 387
Db 361 TSNHNSKKGHCHQBPASLEKOLGCCIE 387

Search completed: October 20, 2005, 06:03:07
Job time : 72 secs

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OM protein - protein search, using sw model

Run on: October 20, 2005, 06:02:31 ; Search time 4754 Seconds
(without alignments)
33.986 Million cell updates/sec

Title: US-10-800-249-2

Perfect score: 2081

Sequence: 1 MNRHLLQDHFLEIDKKNCCV.....KGHCQBPASLEKQLGCCIE 387

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2081	100.0	387	18	US-10-800-249-2
2	1996	95.9	387	15	US-09-930-334-2
3	1996	95.9	387	15	US-10-619-141-2
4	1995	95.9	387	15	US-10-295-027-224
5	1995	95.9	387	15	US-10-188-832-108
6	1995	95.9	625	17	US-10-505-486-86
7	1990	95.6	387	9	US-09-944-807-21
8	1990	95.6	387	14	US-10-092-135-8
9	1990	95.6	387	14	US-10-251-385-108
10	1990	95.6	387	14	US-10-240-842-4
11	1990	95.6	387	14	US-10-225-567A-281

12	1990	95.6	387	14	US-10-296-223-4	Sequence 4, Appli
13	1990	95.6	387	14	US-10-348-083-3	Sequence 3, Appli
14	1990	95.6	387	14	US-10-044-643-43	Sequence 43, Appli
15	1990	95.6	387	15	US-10-295-027-228	Sequence 228, App
16	1990	95.6	387	16	US-10-314-048A-135	Sequence 135, App
17	1990	95.6	387	16	US-10-789-241-6	Sequence 6, Appli
18	1990	95.6	387	16	US-10-874-015-21	Sequence 21, Appli
19	1990	95.6	387	17	US-10-897-815-135	Sequence 135, App
20	1990	95.6	387	18	US-10-930-662-135	Sequence 135, App
21	1990	95.6	387	18	US-10-800-249-3	Sequence 3, Appli
22	1988	95.5	387	14	US-10-251-385-222	Sequence 222, App
23	1935	93.0	363	14	US-10-321-807-36	Sequence 36, Appli
24	1935	93.0	363	15	US-10-295-027-226	Sequence 226, App
25	1935	93.0	363	15	US-10-292-798-668	Sequence 668, App
26	1935	93.0	363	16	US-10-321-807-36	Sequence 36, Appli
27	1935	93.0	363	16	US-10-314-048A-36	Sequence 36, Appli
28	1935	93.0	363	17	US-10-897-815-36	Sequence 36, Appli
29	1935	93.0	363	18	US-10-930-662-36	Sequence 36, Appli
30	1935	93.0	363	18	US-10-800-249-4	Sequence 4, Appli
31	1930	92.7	363	10	US-09-930-334-16	Sequence 16, Appli
32	1930	92.7	363	15	US-10-619-141-16	Sequence 16, Appli
33	1921	92.3	363	16	US-10-314-048A-159	Sequence 159, App
34	1921	92.3	363	17	US-10-897-815-159	Sequence 159, App
35	1921	92.3	363	18	US-10-930-662-159	Sequence 159, App
36	1871	89.9	363	16	US-10-484-788-12	Sequence 12, Appli
37	1864	89.6	392	14	US-10-017-161-808	Sequence 808, App
38	1858	89.3	364	14	US-10-017-161-766	Sequence 766, App
39	1717	82.5	339	14	US-10-188-149A-4	Sequence 4, Appli
40	1670	80.2	363	16	US-10-484-788-14	Sequence 14, Appli
41	1591	76.5	360	16	US-10-484-788-10	Sequence 10, Appli
42	1577	75.8	360	14	US-10-044-643-44	Sequence 44, Appli
43	1577	75.8	360	16	US-10-314-048A-137	Sequence 137, App
44	1577	75.8	360	16	US-10-484-788-8	Sequence 8, Appli
45	1577	75.8	360	17	US-10-897-815-137	Sequence 137, App

ALIGNMENTS

RESULT 1

US-10-800-249-2
; Sequence 2, Application US/10800249
; Publication No. US20050227239A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: VARIANT OF HM74, HGPBMV74
; FILE REFERENCE: D0323 NP
; CURRENT APPLICATION NUMBER: US/10/800,249
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: U.S. 60/454,942
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-800-249-2

Query Match	100.0%;	Score	2081;	DB	18;	Length	387;
Best Local Similarity	100.0%;	Pred. No.	5e-179;				
Matches	387;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVVLGFIPLGLNGLALMIFCFLKSWK	60				
Db	1	MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVVLGFIPLGLNGLALMIFCFLKSWK	60				
Qy	61	SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCLRMLFMLAMNRQGSIIFLT	120				
Db	61	SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCLRMLFMLAMNRQGSIIFLT	120				
Qy	121	VADRYFRVVRVPHALNKNISNRTAIISCLLWGITIGLVHLLKKKMPIQNGGANLCSF	180				

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Db 121 VAVDRYFRVPHALNKNISNRATAIISCLLWGITGLTVHLLKKKMPIONGGANLCSSF 180
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QY 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMSMLDPVVYYFSSPS 300
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QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
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QY 361 TSNNHKKKGHCHOEPASLEKQLGCCIE 387
Db 361 TSNNHKKKGHCHOEPASLEKQLGCCIE 387

RESULT 2
US-09-930-334-2
; Sequence 2, Application US/09930334
; Publication No. US20030078218A1
; GENERAL INFORMATION:
; APPLICANT: Gabor Jarai and Shida Yousefi
; TITLE OF INVENTION: Inflammation related G-protein coupled receptor
; FILE REFERENCE: 4-31553A/HO 33
; CURRENT APPLICATION NUMBER: US/09/930,334
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-334-2
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Query Match 95.9%; Score 1996; DB 10; Length 387;
Best Local Similarity 96.1%; Pred. No. 2.3e-171;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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Db 61 SSRIFLNLAVADFLIIICLPFVMDYVRRSDWKFGDIPCRVLVLFMFAMNRQGSIIFLT 120
QY 121 VAVDRYFRVPHALNKNISNRATAIISCLLWGITGLTVHLLKKKMPIONGGANLCSSF 180
Db 121 VAVDRYFRVPHALNKNISNRATAIISCLLWGITGLTVHLLKKKMPIONGGANLCSSF 180
QY 181 SICHTFQWHEAMFLLFFPLGLIILFCSARIISLQRQMDRHAQIKRAITFTIMVAIVF 240
Db 181 SICHTFQWHEAMFLLFFPLGLIILFCSARIISLQRQMDRHAQIKRAITFTIMVAIVF 240
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RESULT 3
US-10-619-141-2
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; Sequence 2, Application US/10619141
; Publication No. US20040038895A1
; GENERAL INFORMATION:
; APPLICANT: Gabor Jarai and Shida Yousefi
; TITLE OF INVENTION: Inflammation related G-protein coupled receptor
; FILE REFERENCE: 4-31553A/HO 33
; CURRENT APPLICATION NUMBER: US/10/619,141
; CURRENT FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-141-2

Query Match 95.9%; Score 1996; DB 15; Length 387;
Best Local Similarity 96.1%; Pred. No. 2.3e-171;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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QY 61 SSRIFLNLAVADFLIIICLPFLMDNYVRRWDKFGDIPCRMLFMLAMNRQGSIIFLT 120
Db 61 SSRIFLNLAVADFLIIICLPFVMDYVRRSDWKFGDIPCRVLVLFMFAMNRQGSIIFLT 120
QY 121 VAVDRYFRVPHALNKNISNRATAIISCLLWGITGLTVHLLKKKMPIONGGANLCSSF 180
Db 121 VAVDRYFRVPHALNKNISNRATAIISCLLWGITGLTVHLLKKKMPIONGGANLCSSF 180
QY 181 SICHTFQWHEAMFLLFFPLGLIILFCSARIISLQRQMDRHAQIKRAITFTIMVAIVF 240
Db 181 SICHTFQWHEAMFLLFFPLGLIILFCSARIISLQRQMDRHAQIKRAITFTIMVAIVF 240
QY 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMSMLDPVVYYFSSPS 300
Db 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMSMLDPVVYYFSSPS 300
QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
Db 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
QY 361 TSNNHKKKGHCHOEPASLEKQLGCCIE 387
Db 361 TSNNHKKKGHCHOEPASLEKQLGCCIE 387

RESULT 4
US-10-295-027-224
; Sequence 224, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Bos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
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; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 224
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-224

Query Match      95.9%; Score 1995; DB 15; Length 387;
Best Local Similarity 96.1%; Pred. No. 2.8e-171;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHLEIDKKNCCVFRDDFIKVLPPVGLGFIKLLGNGLALMIFCFHLKSWK 60
Db 1 MNRHLLQDHLEIDKKNCCVFRDDFIKVLPPVGLGFIKLLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLNLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120
Db 61 SSRIFLNLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120

Qy 121 VADRYFRVPHPHALNKISNRTAAIISCLLWGTIGLTVHLLKKKMPIONGGANLCSF 180
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Db 181 SICHTFOWHEAMFLEFLPLGIILFCSARIISLQROQMDRHAQIKRAITFINVVAIVF 240

Qy 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLISFTYMSMLDPVVVYFSSPS 300
Db 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLISFTYMSMLDPVVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSCEPWSYILGP 360
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Qy 361 TSNHSHKKGCHQEPASLEKLGCCIE 387
Db 361 TSNHSHKKGCHQEPASLEKLGCCIE 387

RESULT 5
US-10-188-832-108
; Sequence 108, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: MacK, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; PRIOR FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
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; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-108

Query Match      95.9%; Score 1995; DB 15; Length 387;
Best Local Similarity 96.1%; Pred. No. 2.8e-171;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHLEIDKKNCCVFRDDFIKVLPPVGLGFIKLLGNGLALMIFCFHLKSWK 60
Db 1 MNRHLLQDHLEIDKKNCCVFRDDFIKVLPPVGLGFIKLLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLNLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120
Db 61 SSRIFLNLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIIFLTV 120

Qy 121 VADRYFRVPHPHALNKISNRTAAIISCLLWGTIGLTVHLLKKKMPIONGGANLCSF 180
Db 121 VADRYFRVPHPHALNKISNRTAAIISCLLWGTIGLTVHLLKKKMPIONGGANLCSF 180

Qy 181 SICHTFOWHEAMFLEFLPLGIILFCSARIISLQROQMDRHAQIKRAITFINVVAIVF 240
Db 181 SICHTFOWHEAMFLEFLPLGIILFCSARIISLQROQMDRHAQIKRAITFINVVAIVF 240

Qy 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLISFTYMSMLDPVVVYFSSPS 300
Db 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLISFTYMSMLDPVVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSCEPWSYILGP 360
Db 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSCEPWSYILGP 360

Qy 361 TSNHSHKKGCHQEPASLEKLGCCIE 387
Db 361 TSNHSHKKGCHQEPASLEKLGCCIE 387

RESULT 6
US-10-505-486-86
; Sequence 86, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 86
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-86
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Query Match 95.9%; Score 1995; DB 17; Length 625;
Best Local Similarity 96.1%; Pred. No. 5e-171;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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DB 1 MNRHLLQDHLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCRLLMFLMANNRQSGIIFLTV 120
DB 61 SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCRLLMFLMANNRQSGIIFLTV 120

QY 121 VAVDRYFRVVPHHALNKISNRTAAIISCLLWGITTIGLTVHLLKKKMPIONGGANLCSSF 180
DB 121 VAVDRYFRVVPHHALNKISNRTAAIISCLLWGITTIGLTVHLLKKKLLQNGPANVCISF 180

QY 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240
DB 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300
DB 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300

QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360

QY 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387
DB 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387

RESULT 7
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-21

Query Match 95.6%; Score 1990; DB 9; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHLLQDHLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
DB 1 MNRHLLQDHLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCRLLMFLMANNRQSGIIFLTV 120
DB 61 SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCRLLMFLMANNRQSGIIFLTV 120

QY 121 VAVDRYFRVVPHHALNKISNRTAAIISCLLWGITTIGLTVHLLKKKMPIONGGANLCSSF 180
DB 121 VAVDRYFRVVPHHALNKISNRTAAIISCLLWGITTIGLTVHLLKKKLLQNGPANVCISF 180

QY 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240
DB 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300
DB 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300

QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360

QY 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387
DB 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387

Db 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240
QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300
Db 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300
QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360
Db 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360
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RESULT 8
US-10-092-135-8
; Sequence 8, Application US/10092135
; Publication No. US20030054374A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
; FILE REFERENCE: D0134.NP
; CURRENT APPLICATION NUMBER: US/10/092,135
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/273,808
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/278,983
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 387
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-092-135-8

Query Match 95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHLLQDHLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
DB 1 MNRHLLQDHLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

QY 61 SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCRLLMFLMANNRQSGIIFLTV 120
DB 61 SSRIFLNLAVADFLIICLPFLMDNVYVRWDKFGDIPCRLLMFLMANNRQSGIIFLTV 120

QY 121 VAVDRYFRVVPHHALNKISNRTAAIISCLLWGITTIGLTVHLLKKKMPIONGGANLCSSF 180
DB 121 VAVDRYFRVVPHHALNKISNRTAAIISCLLWGITTIGLTVHLLKKKLLQNGPANVCISF 180

QY 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240
DB 181 SICTHFWHEAMFLLFFPLGLIILFCSARIIWSLRQQRMDRHAQIKRAITFTIMVVAIVF 240

QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300
DB 241 VICFLPSVVVIRIFWLLHTSGTQNCVRSVDLAFITLSFTYMNMSMLDPVVYYFSSPS 300

QY 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKWTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360

QY 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387
DB 361 TSNNHKKKGCHQEPASLEKQLGCCIE 387

RESULT 9
US-10-251-385-108

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; Sequence 108, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-251-385-108

Query Match          95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120
Db 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120

Qy 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180
Db 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180

Qy 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240
Db 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240

Qy 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300
Db 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360
Db 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360

Qy 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387
Db 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387

RESULT 11
US-10-240-842-4
; Sequence 281, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 281
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-281

Query Match          95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120
Db 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120

Qy 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180
Db 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180

Qy 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240
Db 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240

Qy 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300
Db 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360
Db 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360

Qy 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387
Db 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387

RESULT 10
US-10-240-842-4
; Sequence 4, Application US/10240842
; Publication No. US20030109673A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 4974.00883
; CURRENT APPLICATION NUMBER: US/10/240,842
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/194,701
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-240-842-4
Query Match          95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120
Db 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120

Qy 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180
Db 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180

Qy 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240
Db 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240

Qy 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300
Db 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360
Db 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360

Qy 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387
Db 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387

RESULT 11
US-10-225-567A-281
; Sequence 281, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 281
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-281

Query Match          95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKKNCCVFRDDFIKVLPPVLGLGFIFGLLGNGLALMIFCFHLKSWK 60

Qy 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120
Db 61 SSRIFLENLAVADFLLIICLPFLMDNVYRRWDKFGDIPCLRLMFLMLAMNRQGSIIIFLTV 120

Qy 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180
Db 121 VAVDRYFRVPHPHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSSF 180

Qy 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240
Db 181 SICTFQWHEAMFLLEFFLPGLIIFCSARIISLRLQROMDRHAQIKRAITFIMVAIVF 240

Qy 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300
Db 241 VICFLPSVVVRIREFWLLHTSGTQNCVYRSVDLAFITILSFTYNNMMLDPVVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360
Db 301 FPNFFSTLINRCLQKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPPSPSYLGP 360

Qy 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387
Db 361 TSNNHKKKGCHQBPASLEKOLGCCIE 387
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QY 181 SICHTFQWHEAMFLLEFFPLGLIILFCSARIIWSLRQQRQDRHAKIKRAITFTIMVVAIVF 240
DB 181 SICHTRFWHEAMFLLEFFPLGLIILFCSARIIWSLRQQRQDRHAKIKRAITFTIMVVAIVF 240
QY 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300
DB 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300
QY 301 FPNFFSTLINRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
QY 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387
DB 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387

RESULT 12
US-10-296-223-4
; Sequence 4, Application US/10296223
; Publication No. US20030139343A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: Lio 080 foreign countries
; CURRENT APPLICATION NUMBER: US/10/296,223
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/208,912
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-223-4
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Query Match 95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLODHLEIDKKNCCVFRDDFTVKVLPVVLGLEFTFGLLGNGLALWIFCFHLKSWK 60
DB 1 MNRHHLODHLEIDKKNCCVFRDDFTAKVLPVVLGLEFTFGLLGNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLIICLPFLMDNYVRRDWKFGDIPCRLLMFLMAMNROGSIIFLTV 120
DB 61 SSRIFLNLAVADFLIICLPFVMDYVRRSDWNFGDIPCRLLVLFMFAMNROGSIIFLTV 120
QY 121 VAVDRYFRVVPVPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIQNGGANLCSF 180
DB 121 VAVDRYFRVVPVPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIQNGPANVCISF 180
QY 181 SICHTFQWHEAMFLLEFFPLGLIILFCSARIIWSLRQQRQDRHAKIKRAITFTIMVVAIVF 240
DB 181 SICHTRFWHEAMFLLEFFPLGLIILFCSARIIWSLRQQRQDRHAKIKRAITFTIMVVAIVF 240
QY 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300
DB 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300
QY 301 FPNFFSTLINRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
QY 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387
DB 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387
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, RESULT 13

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US-10-348-083-3
; Sequence 3, Application US/10348083
; Publication No. US20030186873A1
; GENERAL INFORMATION:
; APPLICANT: EISHINGDELO, Haifeng
; APPLICANT: CAI, Jigong
; APPLICANT: SANDRASAGRA, Anthony
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A G-PROTEIN COUPLED RECEPTOR, AND USES THEREOF
; FILE REFERENCE: USAV2001/0054 US NP
; CURRENT APPLICATION NUMBER: US/10/348,083
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 06/351,001
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: GB 0210597.1
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-083-3

Query Match 95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLODHLEIDKKNCCVFRDDFTVKVLPVVLGLEFTFGLLGNGLALWIFCFHLKSWK 60
DB 1 MNRHHLODHLEIDKKNCCVFRDDFTAKVLPVVLGLEFTFGLLGNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLIICLPFLMDNYVRRDWKFGDIPCRLLMFLMAMNROGSIIFLTV 120
DB 61 SSRIFLNLAVADFLIICLPFVMDYVRRSDWNFGDIPCRLLVLFMFAMNROGSIIFLTV 120
QY 121 VAVDRYFRVVPVPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIQNGGANLCSF 180
DB 121 VAVDRYFRVVPVPHALNKISNRTAAIISCLLWGITTGLTVHLLKKKMPIQNGPANVCISF 180
QY 181 SICHTFQWHEAMFLLEFFPLGLIILFCSARIIWSLRQQRQDRHAKIKRAITFTIMVVAIVF 240
DB 181 SICHTRFWHEAMFLLEFFPLGLIILFCSARIIWSLRQQRQDRHAKIKRAITFTIMVVAIVF 240
QY 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300
DB 241 VICFLPSVVVRIIRIFWLLHTSGTQNCVYRSVDLAFFITLSFTYMNMLDPVVVYFSSPS 300
QY 301 FPNFFSTLINRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
DB 301 FPNFFSTLINRCLQRKWTGPDNNRSTSVELTGDPNKTRGAPALMANSGEPMSPSYLGP 360
QY 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387
DB 361 TSNNHKKGHCHQEPASLEKQLGCCIE 387

RESULT 14
US-10-044-643-43
; Sequence 43, Application US/10044643
; Publication No. US20030195335A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam R
; APPLICANT: Spaderna, Steven K
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishnu, Vieshun S
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Gusev, Vladimir
```

; TITLE OF INVENTION: No. US20030195335a1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-748
; CURRENT APPLICATION NUMBER: US/10/044,643
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/221,284
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/221,325
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/224,588
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/239,613
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/262,508
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,604
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,433
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/265,161
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-643-43

Query Match 95.6%; Score 1990; DB 14; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKKNCCVFRDDFIAKVLPPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy 61 SSRIFLNLAVADFLLIICLPFLMDNVYVRWDKFGDIPCLMLFMLAMNRQSGIIFLTV 120
Db 61 SSRIFLNLAVADFLLIICLPFLMDNVYVRWDKFGDIPCLMLFMLAMNRQSGIIFLTV 120

Qy 121 VAVDRYFRVVPHPHALNKISNRRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSF 180
Db 121 VAVDRYFRVVPHPHALNKISNRRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSF 180

Qy 181 SICTFOWHEAMFLLEFPLGILFCSARIINSLRQDRHAKIKRAITFTIMVAIVF 240
Db 181 SICTFOWHEAMFLLEFPLGILFCSARIINSLRQDRHAKIKRAITFTIMVAIVF 240

Qy 241 VICFLPSVVVRIIRIFWLLHSTGQNCVYRSVDLAFFITLSFTYMSMLDPVYVYFSSPS 300
Db 241 VICFLPSVVVRIIRIFWLLHSTGQNCVYRSVDLAFFITLSFTYMSMLDPVYVYFSSPS 300

Qy 301 FPNFFSTLINRCLQKNTGPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360

Db 301 FPNFFSTLINRCLQKNTGPDNNRSTSVELTGDPNKTRGAPEALMANSGEPMSPSYLGP 360
Qy 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387
Db 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387

RESULT 15
US-10-295-027-228
; Sequence 228, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 228
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-228

Query Match 95.6%; Score 1990; DB 15; Length 387;
Best Local Similarity 95.9%; Pred. No. 8e-171;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNRHLLQDHFLEIDKKNCCVFRDDFIVKVLPPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
Db 1 MNRHLLQDHFLEIDKKNCCVFRDDFIAKVLPPVVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy 61 SSRIFLNLAVADFLLIICLPFLMDNVYVRWDKFGDIPCLMLFMLAMNRQSGIIFLTV 120
Db 61 SSRIFLNLAVADFLLIICLPFLMDNVYVRWDKFGDIPCLMLFMLAMNRQSGIIFLTV 120

Qy 121 VAVDRYFRVVPHPHALNKISNRRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSF 180
Db 121 VAVDRYFRVVPHPHALNKISNRRTAAIISCLLWGITIGLTVHLLKKKMPIONGGANLCSF 180

QY	181	SICHTFQWHEAMFLLLEFFLPLGLIILFCSARI IWSLRQMDRHAKIKRAITFIMVVAIVF	240
Db	181	SICHTFRWHEAMFLLLEFFLPLGLIILFCSARI IWSLRQMDRHAKIKRAITFIMVVAIVF	240
QY	241	VICFLPSVVVRIRIFWLLHTSGTQNCCEVYRSVDLAFFITLSFTYMNMLDPVVYFSSPS	300
Db	241	VICFLPSVVVRIRIFWLLHTSGTQNCCEVYRSVDLAFFITLSFTYMNMLDPVVYFSSPS	300
QY	301	FNFFSTLINRCLQRKMTGEPDNNRSTVELTGDPNKTRGAPEALMANSGEPMSPSYLGP	360
Db	301	FNFFSTLINRCLQRKMTGEPDNNRSTVELTGDPNKTRGAPEALMANSGEPMSPSYLGP	360
QY	361	TSNNHSGKGCHQEPASLEKQLGCCIE	387
Db	361	TSNNHSGKGCHQEPASLEKQLGCCIE	387

Search completed: October 20, 2005, 07:52:41
 Job time : 4755 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 20, 2005, 06:00:16 ; Search time 22 Seconds
(without alignments)
1313.145 Million cell updates/sec

Title: US-10-800-249-2
Perfect score: 2081
Sequence: 1 MNRHHLDHLEIDKKNCCV.....KGHCHOEPASLEKQLGCCIE 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1990	95.6	387	4	US-09-170-496D-108
2	1990	95.6	387	4	US-09-944-807-21
3	1988	95.5	387	4	US-09-170-496D-222
4	563	27.1	423	2	US-08-955-713-2
5	559	26.9	476	2	US-08-955-713-4
6	497.5	23.9	319	3	US-09-130-749-2
7	497.5	23.9	319	3	US-09-130-749-2
8	494.5	23.8	319	4	US-09-170-496D-60
9	494.5	23.8	319	4	US-09-170-496D-196
10	427	20.5	362	3	US-08-513-974B-374
11	415	19.9	373	2	US-08-559-524A-4
12	415	19.9	373	3	US-08-749-707-4
13	415	19.9	373	4	US-09-947-922-4
14	407	19.6	373	4	US-09-745-842-14
15	375.5	18.0	309	3	US-09-422-869-20
16	370.5	17.8	346	4	US-09-585-876-2
17	368	17.7	374	4	US-09-745-842-15
18	353.5	17.0	370	3	US-08-781-250-2
19	350.5	16.8	364	4	US-08-148-708-2
20	350	16.8	339	1	US-08-153-848-44
21	350	16.8	339	2	US-08-812-871-3
22	350	16.8	339	3	US-08-299-843A-44
23	350	16.8	339	3	US-09-088-337B-44
24	350	16.8	339	4	US-09-170-496D-32
25	350	16.8	339	5	PCT-US93-11153-44
26	350	16.8	339	5	PCT-US95-07180-2
27	348.5	16.7	391	4	US-09-826-509-463

ALIGNMENTS

RESULT 1

US-09-170-496D-108

; Sequence 108, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; FILE REFERENCE: AREN-0040

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 234

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 108

; LENGTH: 387

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-108

Query Match 95.6%; Score 1990; DB 4; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.1e-164;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy	1	MNRHHLDHLEIDKKNCCVFRDDPIYKVLPPVLGLEFIFGLLGNGLALMIFCFHLKSWK	60
Db	1	MNRHHLDHLEIDKKNCCVFRDDPIYKVLPPVLGLEFIFGLLGNGLALMIFCFHLKSWK	60
Qy	61	SSRIFENLAVADFLIICLPFLMDNVYRRWMDKFGDIPCLRMLFMLANRQGSIIFLT	120
Db	61	SSRIFENLAVADFLIICLPFLMDNVYRRWMDKFGDIPCLRMLFMLANRQGSIIFLT	120
Qy	121	VAVDRYRVVPHHALNKISNRNTAAITISCLLWGTTIGLTVHLLKKKMPIONGGANLCS	180
Db	121	VAVDRYRVVPHHALNKISNRNTAAITISCLLWGTTIGLTVHLLKKKMPIONGGANLCS	180
Qy	181	SICHTFOWHEAMLEFFELPLGILFCSARIISLROROMDRHAKIKRAITFIMVAIVF	240
Db	181	SICHTFOWHEAMLEFFELPLGILFCSARIISLROROMDRHAKIKRAITFIMVAIVF	240
Qy	241	VICFLPSVVVRIIRIFWLLHSTSGTNCVYRSVDLAFITLSFTYMNMLDPVYVYFSSPS	300
Db	241	VICFLPSVVVRIIRIFWLLHSTSGTNCVYRSVDLAFITLSFTYMNMLDPVYVYFSSPS	300
Qy	301	FPNFFSTLINRCLQRKMTGPDNNRSTVELTDPNKTGRAPALMANSBPSPSYLGP	360
Db	301	FPNFFSTLINRCLQRKMTGPDNNRSTVELTDPNKTGRAPALMANSBPSPSYLGP	360
Qy	361	TSNNHSGKHCHQEPASLEKQLGCCIE	387

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Db 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387
|||||
RESULT 2
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. 6773895
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-21

Query Match 95.6%; Score 1990; DB 4; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.1e-164;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLQDHLEIDKKNCCVFRDDFTVKVLPVVLGFEFIFGLLGNGLALWIFCFHLKSWK 60
DB 1 MNRHHLQDHLEIDKKNCCVFRDDFTAKVLPVVLGFEFIFGLLGNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLIIICLPFVMDYVRRDWMKFGDIPCRLLMFLMAMNRQSGIIIFLTV 120
DB 61 SSRIFLNLAVADFLIIICLPFVMDYVRRDWMKFGDIPCRLLMFLMAMNRQSGIIIFLTV 120
QY 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITVGLTVHLLKKKMPIONGGANLCSSF 180
DB 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITVGLTVHLLKKKMPIONGGANLCSSF 180
QY 181 SICTFOWHEAMFLEFFPLGLIIFCSARIISLRQORQMDRHAQIKRAITFTMVVAIVF 240
DB 181 SICTFOWHEAMFLEFFPLGLIIFCSARIISLRQORQMDRHAQIKRAITFTMVVAIVF 240
QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMNMSMLDPVVVYFSSPS 300
DB 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMNMSMLDPVVVYFSSPS 300
QY 301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPSYLG 360
DB 301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPSYLG 360
QY 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387
DB 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387

RESULT 3
US-09-170-496D-222
; Sequence 22, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-222

Query Match 95.5%; Score 1988; DB 4; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.6e-164;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNRHHLQDHLEIDKKNCCVFRDDFTVKVLPVVLGFEFIFGLLGNGLALWIFCFHLKSWK 60
DB 1 MNRHHLQDHLEIDKKNCCVFRDDFTAKVLPVVLGFEFIFGLLGNGLALWIFCFHLKSWK 60
QY 61 SSRIFLNLAVADFLIIICLPFVMDYVRRDWMKFGDIPCRLLMFLMAMNRQSGIIIFLTV 120
DB 61 SSRIFLNLAVADFLIIICLPFVMDYVRRDWMKFGDIPCRLLMFLMAMNRQSGIIIFLTV 120
QY 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITVGLTVHLLKKKMPIONGGANLCSSF 180
DB 121 VAVDRYFRVVPVHPHALNKISNRTAAIISCLLWGITVGLTVHLLKKKMPIONGGANLCSSF 180
QY 181 SICTFOWHEAMFLEFFPLGLIIFCSARIISLRQORQMDRHAQIKRAITFTMVVAIVF 240
DB 181 SICTFOWHEAMFLEFFPLGLIIFCSARIISLRQORQMDRHAQIKRAITFTMVVAIVF 240
QY 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMNMSMLDPVVVYFSSPS 300
DB 241 VICFLPSVVVIRIFWLLHTSGTQNCVYRSVDLAFITLSFTYMNMSMLDPVVVYFSSPS 300
QY 301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPSYLG 360
DB 301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPALMANSGEPSYLG 360
QY 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387
DB 361 TSNHSHKKGCHQEPASLEKQLGCCIE 387

RESULT 4
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5955308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGMA, DERK
; APPLICANT: HALSEY, WENDY
; TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES A HUMAN 7-TRANS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
```



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; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-955-713-2

Query Match      27.1%; Score 563; DB 2; Length 423;
Best Local Similarity 41.8%; Pred. No. 6.7e-41;
Matches 118; Conservative 52; Mismatches 88; Indels 24; Gaps 5;

QY 30 LPPVLGHEFIPLGNGGLAWIFCFHLKSKWSSRIPLFNLAADFLIICLPFLMDNVVR 89
Db 95 LAPILALEFVLGVGNSLAUFICIHTRPMTSNTVFLVSLVAADFLIISNPLRVDYLL 154
QY 90 RWDKFGDIPCLRLMFLMAMNRQGSIIPLTVAVDVRVYVPHHAKLNKISNRTAAIISC 149
Db 155 HETWRFGAACKVNLFWLSTNRTASVVFLLTAIALNRYLVKVVPHVLSRASVGAAARVAG 214
QY 150 LLGMITGLTVHLKKKMPIONGGANLCSSFSI-----CHTFQWHEAMFLLEFFLPLGIIL 205
Db 215 GLMWGILLNGHLL-----LSTFGSPCLSYRVGTPKPSASLRWHQALYLLLEFFLPLALIL 269
QY 206 FCSARIISLRQRMORHAKIKRAITFMVAVIVFVLCFLPSVY---VRIRIFWLLHTSG 262
Db 270 FAIVSIGLITRNGLGQAGQQRAMRVLAHVAVYITCFLPSIFGMSMAVAFWL----- 324
QY 263 TQNCVYRSVDLA---FFITLSTYMNMLDPVYVYFSSPSF 301
Db 325 -----SACRSIDLCTQLFHGSLAFTYLSVLDPLVLYCFSSPNF 362

RESULT 5
US-08-955-713-4
; Sequence 4, Application US/08955713
; Patent No. 595308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMAN, DEK
; APPLICANT: HALSEY, WENDY
; TITLE OF INVENTION: CDNA CLONE HE04D54 THAT ENCODES A HUMAN 7-TRANS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY, FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087

; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-955-713-4

Query Match      26.9%; Score 559; DB 2; Length 476;
Best Local Similarity 41.5%; Pred. No. 1.7e-40;
Matches 117; Conservative 53; Mismatches 88; Indels 24; Gaps 6;

QY 30 LPPVLGHEFIPLGNGGLAWIFCFHLKSKWSSRIPLFNLAADFLIICLPFLMDNVVR 89
Db 6 LAPILALEFVLGVGNSLAUFICIHTRPMTSNTVFLVSLVAADFLIISNPLRVDYLL 65
QY 90 RWDKFGDIPCLRLMFLMAMNRQGSIIPLTVAVDVRVYVPHHAKLNKISNRTAAIISC 149
Db 66 HETWRFGAACKVNLFWLSTNRTASVVFLLTAIALNRYLVKVVPHVLSRASVGAXARVX- 124
QY 150 LLGMITGLTVHLKKKMPIONGGANLCSSFSI-----CHTFQWHEAMFLLEFFLPLGIIL 205
Db 125 --GGIWWGIL--LLNGXLLLTFTSPGSCLSYRVGTPKPSASLRWHQALYLLLEFFLPLALIL 180
QY 206 FCSARIISLRQRMORHAKIKRAITFMVAVIVFVLCFLPSVY---VRIRIFWLLHTSG 262
Db 181 FAIVSIGLITRNGLGQAGQQRAMRVLAHVAVYITCFLPSIFGMSMAVAFWL----- 235
QY 263 TQNCVYRSVDLA---FFITLSTYMNMLDPVYVYFSSPSF 301
Db 236 -----SACRSIDLCTQLFHGSLAFTYLSVLDPLVLYCFSSPNF 273

RESULT 6
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031090
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: ELSHOURBAGY, NABIL
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-Aug-1998
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70513
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
```

```
/ ; TELEFAX: 610-407-0701
/ ; TELEX: 846169
/ ; INFORMATION FOR SEQ ID NO: 2:
/ ; SEQUENCE CHARACTERISTICS:
/ ;   LENGTH: 319 amino acids
/ ;   TYPE: amino acid
/ ;   STRANDEDNESS: single
/ ;   TOPOLOGY: linear
/ ;   MOLECULE TYPE: protein
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-130-749-2

Query Match      23.9%; Score 497.5; DB 3; Length 319;
Best Local Similarity 36.4%; Pred. No. 2.3e-35;
Matches 110; Conservative 56; Mismatches 111; Indels 25; Gaps 5;

QY 33 VLGLEIFGLGNGLALWIFCFHLKSKSSRIFLFLNLAADFLIIICLPFLMDNYVRRWD 92
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 LLGLECGLLGNGLNAVALWTFLFVRVWKPYAVVLLNLALADLLAAACLPFLAAFYLSQA 79
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 93 WKFGDIPCRMLMFLMAMNRQGSIIFTVVAVDRYFRVPHPHALNKISNRTAAIISCLLW 152
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 WHLGRVGCWALRFLDLSRSVGMFLAAVALDRYLRVPHPRKLVNLLSPQAALGVSGLVW 139
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 153 GITIGTIVHLLKKMPIQNGGANLCSFSFISCHTFQ-----WHEAMFLEFFPLPG 202
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 140 LMVALTCGLLISEAQAQS-----TRCHSFYSRADGSGFSIIWQEALSCLQFVLPFG 191
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 203 ILFCSARIISL--RORQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 192 LIVFCNAGIIRALQKRLREPEKPKLQRAQALVTLVVVLFALCFPCFLARV----LMHI 247
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 261 -SGTQNCVYRSVDLAFFITLSTYMNMSMLDPVYVYFSSPFPNFTLINRCLQRKMTG 319
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 248 FQNLGSCRALCAVAHTSDVTGSLTYLHSLNPVYVYCFSSPTFRSSYRVFHTLRGQAA 307
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 320 EP 321
   ||
Db 308 EP 309

RESULT 7
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031344
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: ELSHOURBAGY, NABIL
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
; TITLE OF INVENTION: RECEPTOR (GPR31A)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: RATNER & PRESTIA
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,749
; FILING DATE: 07-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
```

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/ ; REFERENCE/DOCKET NUMBER: GP-70513
/ ; TELECOMMUNICATION INFORMATION:
/ ; TELEPHONE: 610-407-0700
/ ; TELEFAX: 610-407-0701
/ ; TELEX: 846169
/ ; INFORMATION FOR SEQ ID NO: 2:
/ ; SEQUENCE CHARACTERISTICS:
/ ;   LENGTH: 319 amino acids
/ ;   TYPE: amino acid
/ ;   STRANDEDNESS: single
/ ;   TOPOLOGY: linear
/ ;   MOLECULE TYPE: protein
/ ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-130-749-2

Query Match      23.9%; Score 497.5; DB 3; Length 319;
Best Local Similarity 36.4%; Pred. No. 2.3e-35;
Matches 110; Conservative 56; Mismatches 111; Indels 25; Gaps 5;

QY 33 VLGLEIFGLGNGLALWIFCFHLKSKSSRIFLFLNLAADFLIIICLPFLMDNYVRRWD 92
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 LLGLECGLLGNGLNAVALWTFLFVRVWKPYAVVLLNLALADLLAAACLPFLAAFYLSQA 79
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 93 WKFGDIPCRMLMFLMAMNRQGSIIFTVVAVDRYFRVPHPHALNKISNRTAAIISCLLW 152
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 WHLGRVGCWALRFLDLSRSVGMFLAAVALDRYLRVPHPRKLVNLLSPQAALGVSGLVW 139
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 153 GITIGTIVHLLKKMPIQNGGANLCSFSFISCHTFQ-----WHEAMFLEFFPLPG 202
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 140 LMVALTCGLLISEAQAQS-----TRCHSFYSRADGSGFSIIWQEALSCLQFVLPFG 191
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 203 ILFCSARIISL--RORQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 192 LIVFCNAGIIRALQKRLREPEKPKLQRAQALVTLVVVLFALCFPCFLARV----LMHI 247
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 261 -SGTQNCVYRSVDLAFFITLSTYMNMSMLDPVYVYFSSPFPNFTLINRCLQRKMTG 319
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 248 FQNLGSCRALCAVAHTSDVTGSLTYLHSLNPVYVYCFSSPTFRSSYRVFHTLRGQAA 307
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 320 EP 321
   ||
Db 308 EP 309

RESULT 8
US-09-170-496D-60
; Sequence 60, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 60
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-60

Query Match      23.8%; Score 494.5; DB 4; Length 319;
Best Local Similarity 36.1%; Pred. No. 4.3e-35;
Matches 109; Conservative 57; Mismatches 111; Indels 25; Gaps 5;

QY 33 VLGLEIFGLGNGLALWIFCFHLKSKSSRIFLFLNLAADFLIIICLPFLMDNYVRRWD 92
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 LLGLECGLLGNGLNAVALWTFLFVRVWKPYAVVLLNLALADLLAAACLPFLAAFYLSQA 79
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 93 WKFGDIPCRMLMFLMAMNRQGSIIFTVVAVDRYFRVPHPHALNKISNRTAAIISCLLW 152
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```

Db      80  WHLRGVCWALRFLDLSRSVGMAFLAAVALDRYLRVPHRLKVNLLSPQAALGVSGLVW 139
Qy      153  GITIGLTVHLKKKMPQIONGGANLCSFSICHTFQ-----WHEAMFLLEFFPLG 202
Db      140  LLWVALTCPLLISEAQN-----TRCHSFYSRADGSGFSIIWQEAALSCLOFVLFPFG 191
Qy      203  IILFCARIISWL--RORQMDRAKIKRAITFMVVAIVFICPLPSVVVRIIFWLLHT 260
Db      192  LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFPLCFLARV----LMHI 247
Qy      261  -SGTQNCVRSVDLAFITLSTFYNNMMLDPVVVYFSSPFNFFSTLINRCLQRKWTG 319
Db      248  FQNLGSCRALCAVAHSDVTGSLTYLHSVNPVVVYCFSSPTFRSSYRRVFTLGRKGQA 307
Qy      320  EP 321
Db      308  EP 309

RESULT 9
US-09-170-496D-196
; Sequence 196, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-196

Query Match      23.8%; Score 494.5; DB 4; Length 319;
Best Local Similarity 36.1%; Pred. No. 4.3e-35;
Matches 109; Conservative 57; Mismatches 111; Indels 25; Gaps 5;

Qy      33  VLGLEFTFGLLGNGLAWIFCFHLKSWKSRIFLNFNAVADFLLIICLPFLMDNYVRRWD 92
Db      20  LLGLECGLGLGNVAALWTFLFRVWKPYAVYLLNLALADLLLAACPLFAAFYLSQA 79
Qy      93  WKFGDIPCRMLFMLAMNRQGSIFLTVAVDYFRVYVPHPHALNKISNRATAIISCLLW 152
Db      80  WHLRGVCWALRFLDLSRSVGMAFLAAVALDRYLRVPHRLKVNLLSPQAALGVSGLVW 139
Qy      153  GITIGLTVHLKKKMPQIONGGANLCSFSICHTFQ-----WHEAMFLLEFFPLG 202
Db      140  LLWVALTCPLLISEAQN-----TRCHSFYSRADGSGFSIIWQEAALSCLOFVLFPFG 191
Qy      203  IILFCARIISWL--RORQMDRAKIKRAITFMVVAIVFICPLPSVVVRIIFWLLHT 260
Db      192  LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFPLCFLARV----LMHI 247
Qy      261  -SGTQNCVRSVDLAFITLSTFYNNMMLDPVVVYFSSPFNFFSTLINRCLQRKWTG 319
Db      248  FQNLGSCRALCAVAHSDVTGSLTYLHSVNPVVVYCFSSPTFRSSYRRVFTLGRKGQA 307
Qy      320  EP 321
Db      308  EP 309

RESULT 10
US-08-513-974B-374
; Sequence 374, Application US/08513974B
```

```

; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; MOLECULE TYPE: peptide
US-08-513-974B-374

Query Match      20.5%; Score 427; DB 3; Length 362;
Best Local Similarity 29.4%; Pred. No. 3.5e-29;
Matches 97; Conservative 73; Mismatches 132; Indels 28; Gaps 8;

QY 18 CCVRDDFIVKVLPPVVLGIEFIFGLGNGIALWIFCFHLKSKSSRIFLFNLAADFLLI 77
Db 31 CSUTKGFQFYLYPTVILVFIIFGLGNSVAIMWFVHMFKPWSGISVYMFNLALADFLYV 90
QY 78 ICLPFLMDNVRWDKFGDIPCLRLMFLMANNRQSGIIFLTIVVADVFRVVPVPHALN 137
Db 91 LTLPALIFYFYFNKTDWIFGDMCKLQRFIFHVNLYGSIILFTLCISVHRTYGVVHPLKSLG 150
QY 138 KISNRATAIISCLLWGI-TIGLTVHLLKKMPTONGANLCS------FSICH 184
Db 151 RLKKNAVYSSLVWALVAVIAPILFYSGIGVRRNKTTICYDTTADVLRSYFVYSMCT 210
QY 185 TQWHEAMFLLEFPLPLGILFCSARIINSLRQROMDRHAKIKRAITFIMVVAI-VFVIC 243
Db 211 T-----VFMCIFIFVILGCGYGLIVRALIYKDLN-NSPLRKKSTYLVILVITVFAVS 261
QY 244 FLPSVVR-IRIFWLLHTSGTQCEVYRSVDLAFFITLSTFTYNNMLDPVYVYFSSPFP 302
Db 262 YLPHVWKTINLRARLDFTQPMCAFNDKVYATYQVTRGLASINSCVDPILYFLAGDTFR 321
QY 303 NFFSTLINRCLQKMTGEPDNNRSTSVELT 332
Db 322 RLRSRATRKSSRR---SEP-NVQSKSEMT 347

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RESULT 11
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-559-524A-4

Query Match      19.9%; Score 415; DB 3; Length 373;
Best Local Similarity 29.8%; Pred. No. 4e-28;
Matches 98; Conservative 66; Mismatches 139; Indels 26; Gaps 6;

QY 18 CCVRDDFIVKVLPPVVLGIEFIFGLGNGIALWIFCFHLKSKSSRIFLFNLAADFLLI 77
Db 42 CALTKGTFQFYLYPAVYILVFIIFGLGNSVAIMWFVHMFKPWSGISVYMFNLALADFLYV 101
QY 78 ICLPFLMDNVRWDKFGDIPCLRLMFLMANNRQSGIIFLTIVVADVFRVVPVPHALN 137
Db 102 LTLPALIFYFYFNKTDWIFGDMCKLQRFIFHVNLYGSIILFTLCISAHRYSGVYVPLKSLG 161
QY 138 KISNRATAIISCLLWGI-TIGLTVHLLKKMPTONGANLCS------FSICH 184
Db 162 RLKKNAVYISLVWILVVGISPIIFYSGTGIRKKNKTTICYDTTSDVLRSYFYSMCT 221
QY 185 TQWHEAMFLLEFPLPLGILFCSARIINSLRQROMDRHAKIKRAITFIMVVAI-VFVIC 244
Db 222 TV-----AMFC---VPLVLILGCGYGLIVRALIYKDLN-NSPLRKKSTYLVILVITVFAVS 273
QY 245 FLPSVVR-IRIFWLLHTSGTQCEVYRSVDLAFFITLSTFTYNNMLDPVYVYFSSPFP 303
Db 274 IPHVWKTINLRARLDFTQPMCAFNDKVYATYQVTRGLASINSCVDPILYFLAGDTFR 333
QY 304 NFFSTLINRCLQKMTGEPDNNRSTSVELT 332
Db 334 RLRSRATRKSSRR---NLSKSEDMT 358

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Qy 18 CCVRDDFIVKVLPPVGLGFIFGLLGNGLALWIFCFHLKSWKSSRIFFLENLAVADFLI 77
Db 42 CALTKTGQFYFYLPAVYILVFIIGFLGNSVAIWMFVFMKPSGSIYVMFNALADFLYV 101
Qy 78 ICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIFLTVAVDYFRVVPHPHALN 137
Db 102 LTLPALIFYFNKTDWIFGDMCKLQRFIFHVNLYGSILFTLCISAHRYSGVYPLKSLG 161
Qy 138 KISNRTAIISCLLWGI-TIGLTVHLLKKMPKIQNGGANLCS-----FSICH 184
Db 162 RLKKNAVYISVLWLIWVGISPLIFYSGTGIRKNTITCYDTSDEYLSYFIYSMCT 221
Qy 185 TFQWHEAMFLEFFLPLGIILFCSARIISWISURQOMDRHAKIKRAITFIWVAIVFVICF 244
Db 222 TV-----AMFC-----VPLVILGCVGLIVRALIYKDLNLSPLRRKSIYLVIIIVTFVAVSY 273
Qy 245 LPSVVVR-IRIFWLLHTSGTQNCVYRSVDLAPITLSFTYMNMLDPVVYFSPSPFN 303
Db 274 IPFHVMTNLRARLDFQTPMCAPNDRVYATYQVTRGLASLNSCVDPIFLYLAGDTFRR 333
Qy 304 FFSTLINRCLQKMTGEPDNNRSTSVELT 332
Db 334 RLSRATRKASRSEA-----NLQSKSEDMT 358

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RESULT 13
US-09-947-922-4
; Sequence 4, Application US/09947922
; Patent No. 6680373
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,922
; FILING DATE: 07-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-922-4

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Query Match 19.9%; Score 415; DB 4; Length 373;
Best Local Similarity 29.8%; Pred. No. 4e-28;

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Matches 98; Conservative 66; Mismatches 139; Indels 26; Gaps 6;
Qy 18 CCVRDDFIVKVLPPVGLGFIFGLLGNGLALWIFCFHLKSWKSSRIFFLENLAVADFLI 77
Db 42 CALTKTGQFYFYLPAVYILVFIIGFLGNSVAIWMFVFMKPSGSIYVMFNALADFLYV 101
Qy 78 ICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIFLTVAVDYFRVVPHPHALN 137
Db 102 LTLPALIFYFNKTDWIFGDMCKLQRFIFHVNLYGSILFTLCISAHRYSGVYPLKSLG 161
Qy 138 KISNRTAIISCLLWGI-TIGLTVHLLKKMPKIQNGGANLCS-----FSICH 184
Db 162 RLKKNAVYISVLWLIWVGISPLIFYSGTGIRKNTITCYDTSDEYLSYFIYSMCT 221
Qy 185 TFQWHEAMFLEFFLPLGIILFCSARIISWISURQOMDRHAKIKRAITFIWVAIVFVICF 244
Db 222 TV-----AMFC-----VPLVILGCVGLIVRALIYKDLNLSPLRRKSIYLVIIIVTFVAVSY 273
Qy 245 LPSVVVR-IRIFWLLHTSGTQNCVYRSVDLAPITLSFTYMNMLDPVVYFSPSPFN 303
Db 274 IPFHVMTNLRARLDFQTPMCAPNDRVYATYQVTRGLASLNSCVDPIFLYLAGDTFRR 333
Qy 304 FFSTLINRCLQKMTGEPDNNRSTSVELT 332
Db 334 RLSRATRKASRSEA-----NLQSKSEDMT 358

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RESULT 14
US-09-745-842-14
; Sequence 14, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopetter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 4481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
US-09-745-842-14

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```

Query Match 19.6%; Score 407; DB 4; Length 373;
Best Local Similarity 28.5%; Pred. No. 2e-27;
Matches 97; Conservative 62; Mismatches 133; Indels 48; Gaps 7;
Qy 18 CCVRDDFIVKVLPPVGLGFIFGLLGNGLALWIFCFHLKSWKSSRIFFLENLAVADFLI 77
Db 42 CALTKTGQFYFYLPAVYILVFIIGFLGNSVAIWMFVFMKPSGSIYVMFNALADFLYV 101
Qy 78 ICLPFLMDNVYRRWDKFGDIPCLRLMFLMAMNRQGSIIFLTVAVDYFRVVPHPHALN 137
Db 102 LTLPALIFYFNKTDWIFGDMCKLQRFIFHVNLYGSILFTLCISAHRYSGVYPLKSLG 161
Qy 138 KISNRTAIISCLLWGI-TIGLTVHLLKKMPKIQNGGANLCS-----FSICH 184
Db 162 RLKKNAVYISVLWLIWVGISPLIFYSGTGIRKNTITCYDTSDEYLSYFIYSMCT 221
Qy 185 TFQWHEAMFLEFFLPLGIILFCSARIISWISURQOMDRHAKIKRAITFIWVAIVFVICF 244
Db 222 TV-----AMFC-----VPLVILGCVGLIVRALIYKDLNLSPLRRKSIYLVIIIVTFVAVSY 273

```

Qy	245	LPSVVVRIRIFWLLHTSGTON----	CEVRSVDLAFPTLTSTFYVNSMLDPV	292
Db	274	IP-----FHWKTKMLRLARLDEQT	PAMCAFNDRVYATYQVTRGLASLNS	322
Qy	293	VYFSPSPFPNFSTLIQLRCQKMTGPD	NNRSTSVELT	332
Db	323	LYPLAGDTERRLSRATKASRRSEA---	NLOKSEDMT	358

RESULT 15

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US-09-422-869-20
; Sequence 20, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SREENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; CURRENT FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; EARLIER FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-422-869-20

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Query Match	18.0%;	Score	375.5;	DB	3;	Length	309;
Best Local Similarity	34.1%;	Pred. No.	8.6e-25;				
Matches	94;	Conservative	48;	Mismatches	107;	Indels	27;
Gaps	10;						
Qy	34	LGLEFFIQLGGLGIALMIFCFHLKSKSSRRIFLNFNLAVADFLLIICLPFLMDNYVRWDW	93				
Db	27	LGVLVLGILLNLSLAVVFCRMQWTETRIYMTNLAVADLCLLCTLPFVLHSL	81				
Qy	94	KFGDIP-CRLMFLMANNRQGSIIFTVAVDRYFVRVHPHALNKLNRTAAIISCLLW	152				
Db	82	DTSDTPCQLSQSGHYLNRVNSLSVTAIAVDRYAVVRHPLRAGLRSPQAAAVCAVLW	141				
Qy	153	GITIGLTVHLLKKKMPITQNGANLCSFSICHTFQWHEAMF-LLEPFLPLGIILFCSARI	211				
Db	142	VLVIGSLV--ARWLLGIQEG--PCPR-STRHNP--NSMRFLPLGGFLPLAVVVFCSLKV	194				
Qy	212	IWSLRQR--QMDRHAKIKRAIFIMVVAIVFVTCFLP--SVVVRIRIPEWLLHTSTQN	265				
Db	195	VTALQAQPPPTDVGQAETRAARVMWANLIVFVVCFLPHVGLTVRLAVGM-----NA	247				
Qy	266	CEVYRSVDLAFFITLSFTYMSMLDPPVYVFPSSPSF	301				
Db	248	CALLLETTERRALYITSKUSDANCCDAICYYMAKEF	283				

Search completed: October 20, 2005, 06:34:05
Job time : 75 secs